name	symbol	Applied Biosystems "assay on demand" assay #	forward primer	Seq ID No.	reverse primer	Seq ID No.	probe	Seq ID No.
asporin (lrr class 1)	ASPN		AAATACAAAAGGACACATTCAAAGGA	1	TGCTTCTGCAATTCTGATATGGA	23	TTGGAAATGAGTGCAAACCCTCTTGATAATAATG	45
chondroitin sulfate proteoglycan 2 (versican)	CSPG2		GCCAGTGGAATGATGTTCCC	2	TCTTGGCATTTTCTACAACAGGG	24	AGGAACAGTTGCTTGCGGCCAGC	46
cystatins SN, SA & S	CST1, 2, 4		AGTCCCAGCCCAACTTGGA	3	GGGAACTTCGTAGATCTGGAAAGA	25	AGCCAGAACTGCAGAAGAAACAGTTGTGC	47
gamma-glutamyl hydrolase	GGH		GTGGCAATGCCGCTGAA	4	TGACAGCAACAACTCAGTAGGAAAA	26	TTCACTGGAGGTCAATTGCACAGCAGAAT	48
insulin-like growth factor binding protein 7	IGFBP7		CAGGTCAGCAAGGGCACC	5	TCACAGCTCAAGTACACCTGGG	27	AGCAAGGTCCTTCCATAGTGACGCCC	49
kallikrein 10	KLK10		ACAACATGATATGTGCTGGACTGG	6	GAGAGGATGCCTTGGAGGGT	28	CTTGCCAGAGTGACTCTGGAGGCCC	50
leucine proline-enriched proteoglycan 1(leprecan 1)	LEPRE1		CTTGAGTACAACGCTGACCTCTTC	7	CCGTGACACAGTTCTGCTTACAG	29	CCATCACAGATCATTACATCCAGGTCCTCA	51
lumican	LUM		GATTCTTGTCCATAGTGCATCTGC	8	CCAATCAATGCCAGGAAGAGA	30	TAAGGATTCAAACCATTTGCCAAAAATGAGTCTAAG	52
lysyl oxidase-like 2	LOXL2		AGGCCAGCTTCTGCTTGGA	9	CCCTGATCGCCGAGTTG	31	CGTAATTCTTCTGGATGTCTCCTTCACATTCTG	53
matrix metalloproteinase 12	MMP12		GCCTCTCTGCTGATGACATACGT	10	AGTGACAGCATCAAAACTCAAATTG	32	TCAGTCCCTGTATGGAGACCCAAAAGAGAA	54
metalloproteinase inhibitor 1	TIMP1		CCAGACCACCTTATACCAGCG	11	GGACCTGTGGAAGTATCCGC	33	CAAGATGACCAAGATGTATAAAGGGTTCCAAGC	55
n-acylsphingosine amidohydrolase	ASAH1		CGCAGAACGCCTGCAAA	12	ACAGGACATCATACATGGTTTCAAA	34	TGTCTGAACCGCACCAGCCAAGAGAATA	56
secreted frizzled-related protein 2	SFRP2		CGCTAGCAGCGACCACCT	13	TTTTGCAGGCTTCACATACCTTT	35	CTGCCAGCCACCGAGGAAGCTC	57
secreted protein, acidic, cysteine rich	SPARC		TCTTCCCTGTACACTGGCAGTTC	14	GAAAAAGCGGGTGGTGCA	36	TGGACCAGCACCCCATTGACGG	58
serine protease 11 (IGF binding)	PRSS11		TCGGGAGGCCCGTTAGTAA	15	AAGGAGATTCCAGCTGTCACTTTC	37	AGTGTTAATTCCAATCACTTCACCGTCCAGG	59
thrombospondin 2	THBS2		TGGAAGGACTACACGGCCTATAG	16	TAGGTTTGGTCATAGATAGGTCCTGAGT	38	AGGCCCAAGACCGGCTACATCAGAGTC	60
thyroglobulin	TG		GACGGTTCCTCGCAGTTCAA	17	TGTAAACCGCTCCACTTCACAT	39	TCTGGCAGATTCCGATGCCCCACAA	61
human cell growth regulator with EF hand domain 1	CGR11		CTGCCCACCCCTTCCA	18	TTCTGTCCTTCCTAGTCCCTTTAGG	40	CCAGGCCAGGAGCAGCTCGG	62
human serine or cysteine proteinase inhibitor clade B	SERPINB5		TCCACGCATTTTCCAGGATAA	19	AAGCCGAATTTGCTAGTTGCA	41	TGACTCCAGGCCCGCAATGGA	63
transforming growth factor β1	TGFB1		GGTCCATGTCATCACCAATGTT	20	TCTGCAAGTTCATCCCCTCTTT	42	CAGCCTCCAGCCAACAGACCTCAGG	64
human proprotein convertase subtilisin/kexin type 5	PCSK5		AAAAATCTTTGCCGGAAATGC	21	AGTCCTGGCCGTTGAAATACC	43	ACAGAATGTAGGGATGGGTTAAGCCTGCA	65
matrix metalloproteinase 2	MMP2		TTGATGGCATCGCTCAGATC	22	TGTCACGTGGCGTCACAGT	44	TTCAAGGACCGGTTCATTTGGCG	66
human serine or cysteine proteinase inhibitor clade H	SERPINH1	Hs00241844_m1						
adlican	-	Hs00377849_m1						
egf-containing fibulin-like extracellular matrix protein 2	EFEMP2	Hs00213545_m1						
secreted frizzled-related protein 4	SFRP4	Hs00180066_m1						
inhibin beta A chain	INHBA	Hs00170103_m1						
osteopontin	SPP1	Hs00167093_m1						
transforming growth factor B-induced	TGFBI	Hs00165908_m1						
			Figure 1					

Microarray - Identification of Markers for Gastric Malignancy										
name	symbol	MWG oligo #	NCBI mRNA ref sequence	protein ref sequence	fold change	fold change rank	original t-test	Bonferroni-adjusted p value	2 sample Wilcoxon test
adlican	-	C:0531	NM_015419	NP_056234	1.8	-17818	1.0E-28	3.04E-24	0.0E+00
asporin (lrr class 1)	ASPN	A:07749	NM_017680	NP_060150	2.6	-22292	6.4E-23	1.9E-18	0.0E+00
carboxypeptidase N	CPN2	B:4922	-	P22792	2.7	-22367.5	2.3E-42	7.0E-38	0.0E+00
cell growth regulatory factor with EF-hand domain	CGR11	A:07876	NM_006569	NP_006560	3.0	-21188.5	4.33E-42	1.3E-37	0.0E+00
chondroitin sulfate proteoglycan 2 (versican)	CSPG2	A:10008	NM_004385	NP_004376	2.3	-21606.5	2.23E-33	6.65E-29	0.00E+00
cystatin SN	CST1	A:06089	NM_001898	NP_001889	2.1	-17475	1.3E-18	3.8E-14	0.0E+00
cystatin SA	CST2	A:06089	NM_001322	NP_001313	2.1	-17475	1.3E-18	3.8E-14	0.0E+00
cystatin S	CST4	A:06089	NM_001899	NP_001890	2.1	-17475	1.3E-18	3.8E-14	0.0E+00
egf-containing fibulin-like extracellular matrix protein 2	EFEMP2	A:09072	NM_016938	NP_058634	2.4	-22761	2.0E-35	5.9E-31	0.0E+00
gamma-glutamyl hydrolase	GGH	A:03601	NM_003878	NP_003869	1.6	-18092	1.6E-07	4.8E-03	5.7E-11
inhibin beta A chain	INHBA	A:02189	NM_002192	NP_002183	2.1	-21247	1.4E-30	4.3E-26	0.0E+00
insulin-like growth factor binding protein 7	IGFBP7	A:03385	NM_001553	NP_001544	3.0	-25854	5.4E-31	1.6E-26	0.0E+00
kallikrein 10	KLK10	A:07907	NM_002776	NP_002767	2.3	-17986.5	5.0E-10	1.5E-05	4.9E-06
leucine proline-enriched proteoglycan 1(leprecan 1)	LEPRE1	A:04646	NM_022356	NP_071751	1.7	-18019	8.2E-14	2.4E-09	1.1E-12
lumican	LUM	A:09199	NM_002345	NP_002336	2.9	-24927	4.2E-24	1.3E-19	0.0E+00
lysyl oxidase-like 2	LOXL2	A:06085	NM_002318	NP_002309	1.6	-16994.5	5.9E-10	1.7E-05	7.9E-10
matrix metalloproteinase 2	MMP2	A:06749	NM_004530	P08253	1.8	-18710	1.2E-11	3.6E-07	1.5E-10
matrix metalloproteinase 12	MMP12	A:01762	NM_002426	NP_002417	2.1	-20209.5	2.2E-12	6.6E-08	4.9E-11
metalloproteinase inhibitor 1	TIMP1	A:08048	NM_003254	NP_003245	3.2	-24177	7.5E-38	2.3E-33	0.0E+00
n-acylsphingosine amidohydrolase	ASAH1	A:10030	NM_004315	NP_004306	1.7	-19636.5	9.6E-16	2.9E-11	0.0E+00
olfactomedin	OLFM1	B:3555	NM_014279	NP_055094	3.9	-25782.5	6.5E-46	1.9E-41	0.0E+00
osteopontin	SPP1	A:09441	NM_000582	NP_000573	7.0	-26668	4.0E-32	1.2E-27	0.0E+00
human proprotein convertase subtilisin/kexin type 5	PCSK5	A:00704	NM_006200	Q92824	1.7	-18736	2.0E-11	6.0E-07	7.3E-11
group xiii secreted phospholipase a2	PLA2G12b	B:1811	NM_032562	NP_115951	3.0	-23212	7.92E-39	2.36E-34	0.00E+00
secreted frizzled-related protein 2	SFRP2	B:1634	XM_050625	XP_050625	2.1	-19217	2.7E-10	8.1E-06	4.1E-08
secreted frizzled-related protein 4	SFRP4	A:07398	NM_003014	NP_003005	3.0	-22153	6.0E-24	1.8E-19	0.0E+00
serine (or cysteine) proteinase inhibitor clade H	SERPINH1	A:08615	NM_001235	NP_001226	1.9	-20252	2.8E-34	8.2E-30	0.0E+00
human serine or cysteine proteinase inhibitor clade B	SERPINB5	A:10485	NM_002639	P36952	1.5	-17026	4.6E-06	1.4E-01	5.6E-06
serine protease 11 (IGF binding)	PRSS11	B:1274	NM_002775	NP_002766	1.6	-17184.5	9.3E-18	2.8E-13	0.0E+00
secreted protein, acidic, cysteine rich	SPARC	A:08092	NM_003118	NP_003109	2.5	-22947.5	1.5E-44	4.6E-40	0.0E+00
spondin 2	SPON2	B:2543	NM_012445	NP_036577	2.4	-20390.5	2.9E-31	8.5E-27	0.0E+00
stannin	SNN	A:09316	NM_003498	NP_003489	2.1	-20162.5	3.25E-24	9.71E-20	0.00E+00
thrombospondin 2	THBS2	B:9017	NM_003247	NP_003238	2.6	-22095	5.8E-29	1.7E-24	0.0E+00
thrombospondin repeat containing 1	TSRC1	B:7686	NM_019032	NP_061905	2.6	-22608	1.38E-45	4.1E-41	0.0E+00
thyroglobulin	TG	B:5402	NM_003235	NP_003226	2.4	-23644	4.39E-36	1.3E-31	0.0E+00
transforming growth factor β-induced	TGFBI	A:08124	NM_000358	NP_000349	2.5	-23339.5	1.96E-24	9.71E-20	0.0E+00
transforming growth factor β1	TGFB1	A:07050	NM_000660	P01137	1.6	-17214	2.30E-18	6.86E-14	0.0E+00
hyaluronan and proteoglycan link protein 4	HAPLN4	C:6300	NM_023002	NP_075378	3.4	-23516.5	7.32E-44	2.2E-39	0.0E+00

Figure 2

Quantitative RT-PCR - Quantification of Expression of Selected Gastric Cancer Candidate Genes					
name	symbol	median T:N fold change	Maximum T:N fold change	% T >95th percentile [1]	
adlican		5	37	74	
asporin (lrr class 1)	ASPN	12	73	91	
chondroitin sulfate proteoglycan 2 (versican)	CSPG2	6	24	78	
cystatins SN, SA & S	CST1, 2, 4	525	25532	100	
egf-containing fibulin-like extracellular matrix protein 2	EFEMP2	3	15	56	
gamma-glutamyl hydrolase	GGH	5	36	67	
inhibin beta A chain	INHBA	34	357	98	
insulin-like growth factor binding protein 7	IGFBP7	4	19	80	
kallikrein 10	KLK10	5	633	70	
leucine proline-enriched proteoglycan 1(leprecan 1)	LEPRE1	4	17	72	
lumican	LUM	5	47	80	
lysyl oxidase-like 2	LOXL2	6	26	93	
matrix metalloproteinase 12	MMP12	9	586	67	
metalloproteinase inhibitor 1	TIMP1	8	19	91	
n-acylsphingosine amidohydrolase	ASAH1	3	7	63	
osteopontin	SPP1	40	481	96	
secreted frizzled-related protein 2	SFRP2	5	85	63	
secreted frizzled-related protein 4	SFRP4	56	600	100	
secreted protein, acidic, cysteine rich	SPARC	9	56	93	
serine protease 11 (IGF binding)	PRSS11	4	25	54	
thrombospondin 2	THBS2	25	239	91	
thyroglobulin	TG	5	153	54	
transforming growth factor B-induced	TGFBI	7	204	82	
[1] percentage of tumors with expression levels greater than the 95th percentile of non-malignant samples.					

Figure 3

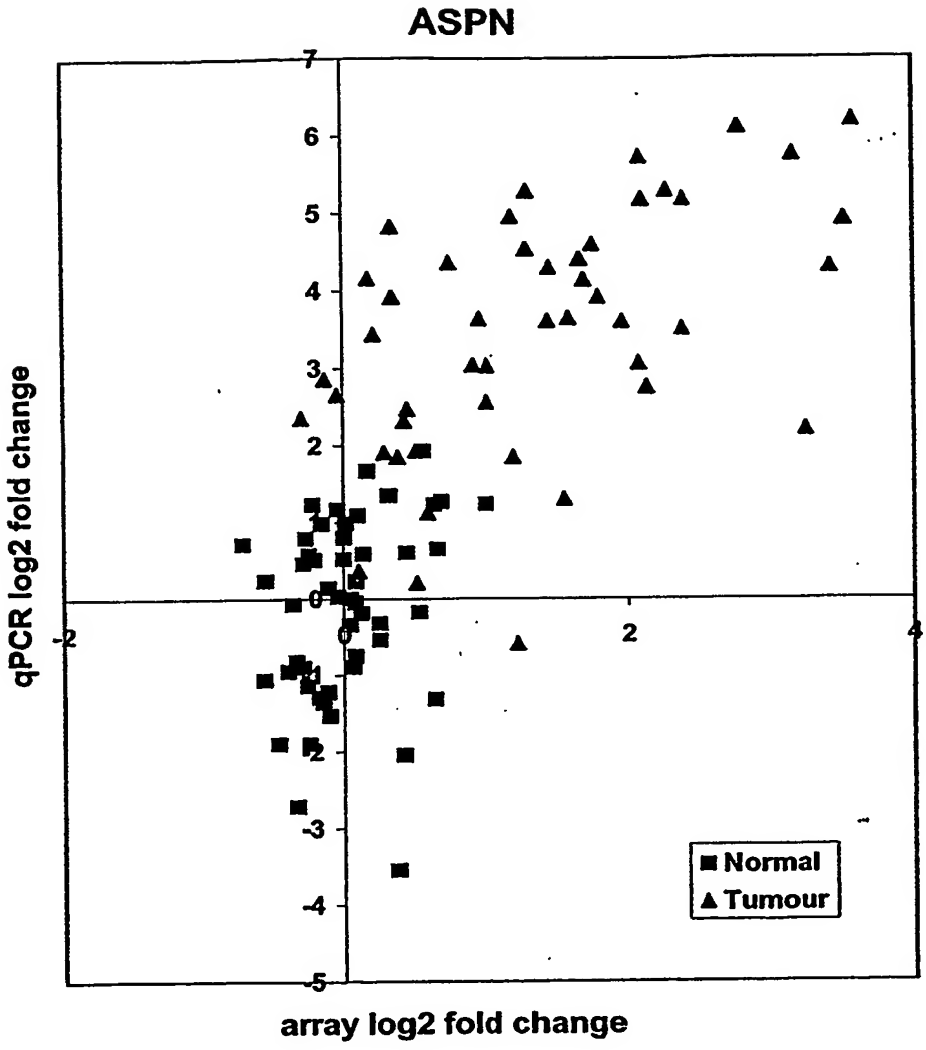

ASPN
qPCR log2 fold change
array log2 fold change
Normal
Tumour
7
6
5
4
3
2
0
-1
-2
-3
-4
-5
-2
2
4

Figure 4(a)

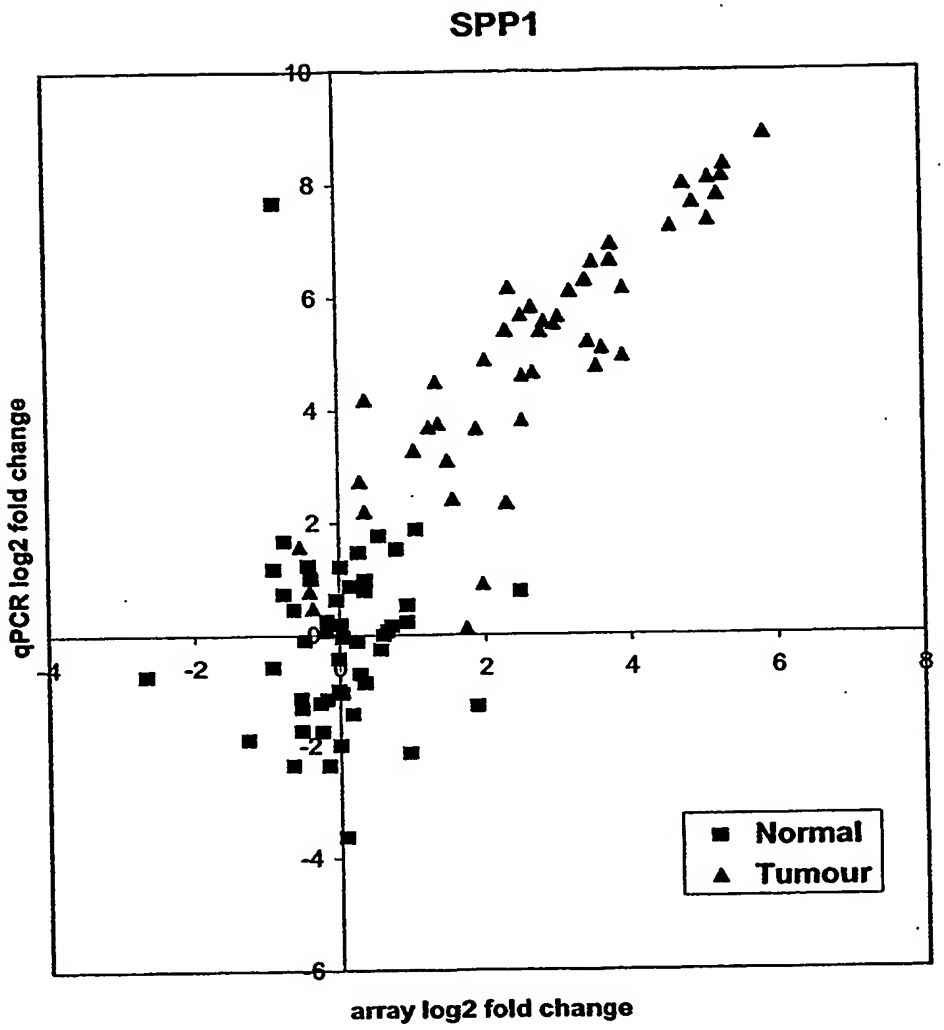

SPP1
qPCR log2 fold change
array log2 fold change
Normal
Tumour
10
8
6
4
2
0
-2
-4
-6
-4
-2
0
2
4
6
8

Figure 4(b)

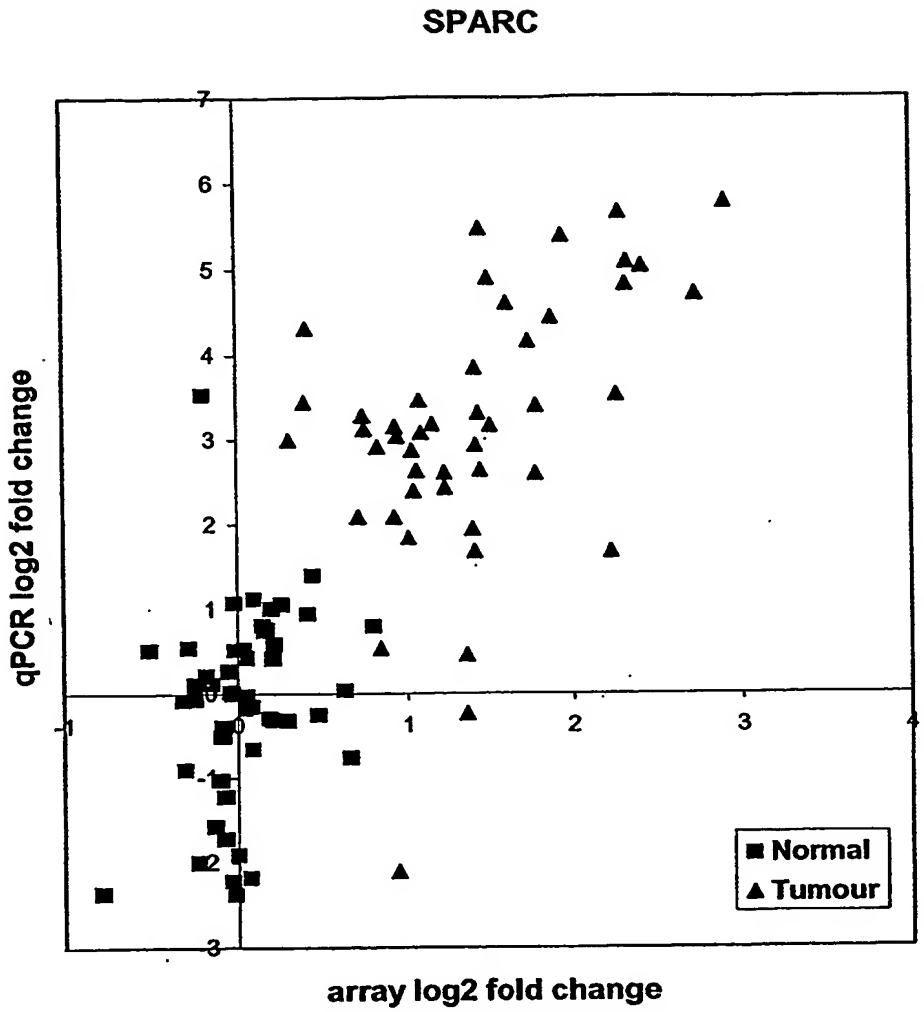
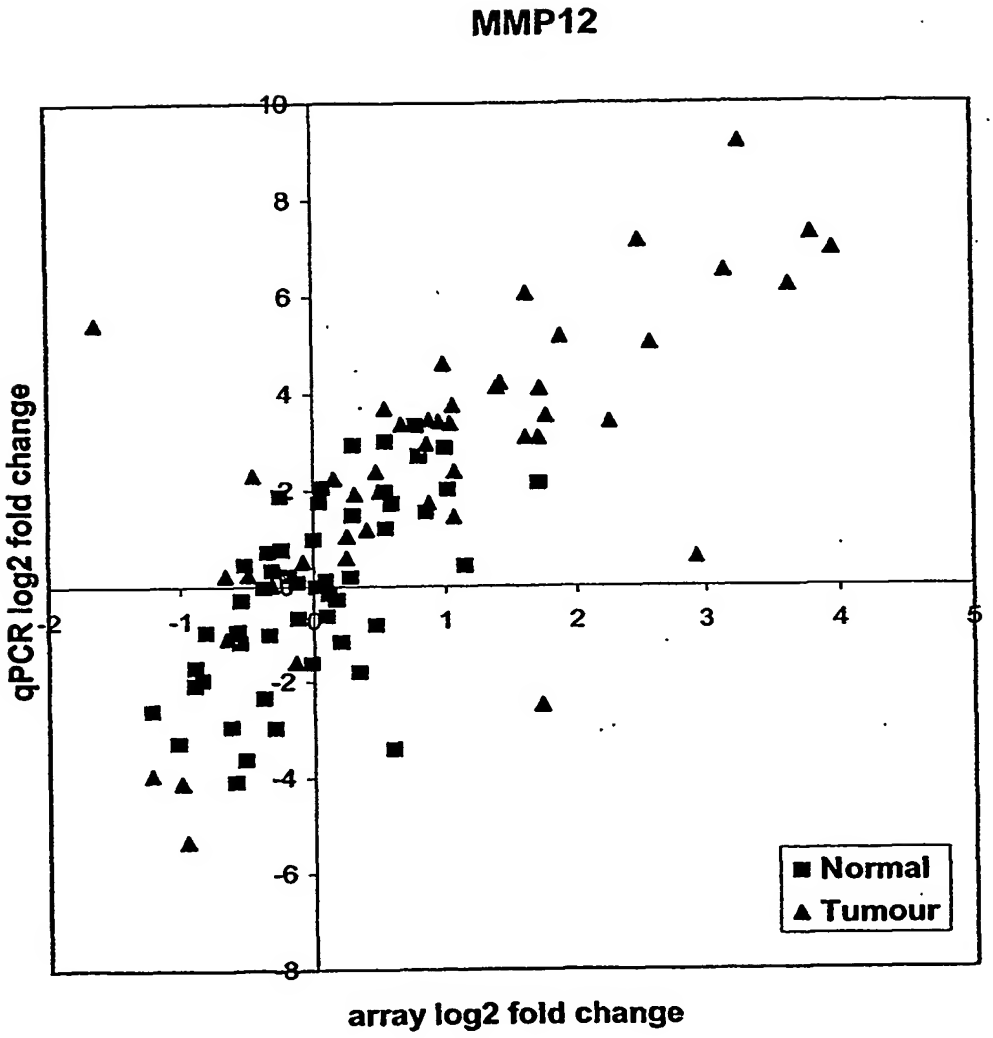

SPARC
qPCR log2 fold change
array log2 fold change
Normal
Tumour

Figure 4(c)


MMP12
qPCR log2 fold change
array log2 fold change
Normal
Tumour
10
8
6
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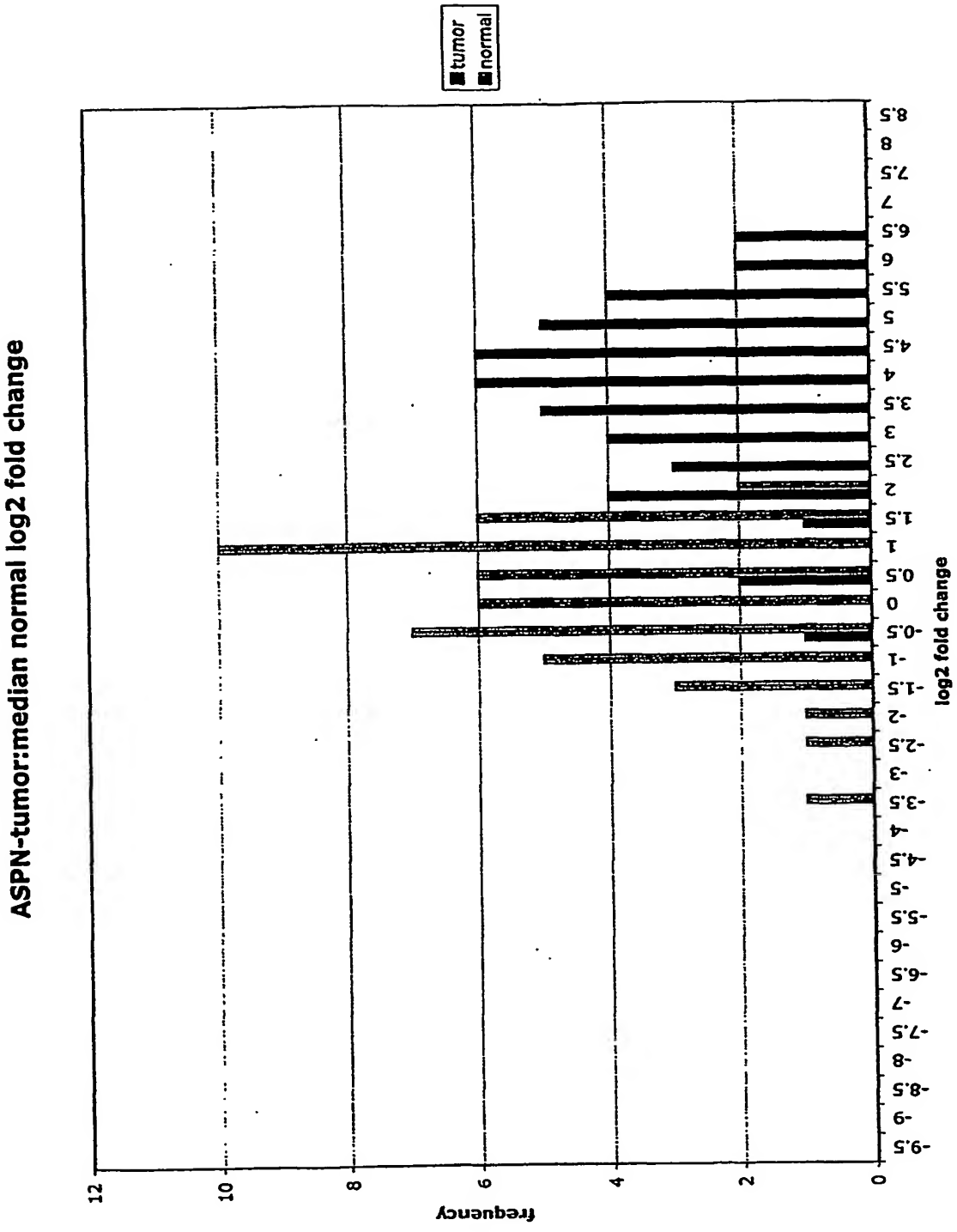
2
0
-2
-4
-6
-8
-2
-1
0
1
2
3
4
5

Figure 4(d)


ASPN-tumor:median normal log2 fold change
tumor
normal
frequency
log2 fold change
12
10
8
6
4
2
0
8.5
8
7.5
7
6.5
6
5.5
5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
-2.5
-3
-3.5
-4
-4.5
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-6.5
-7
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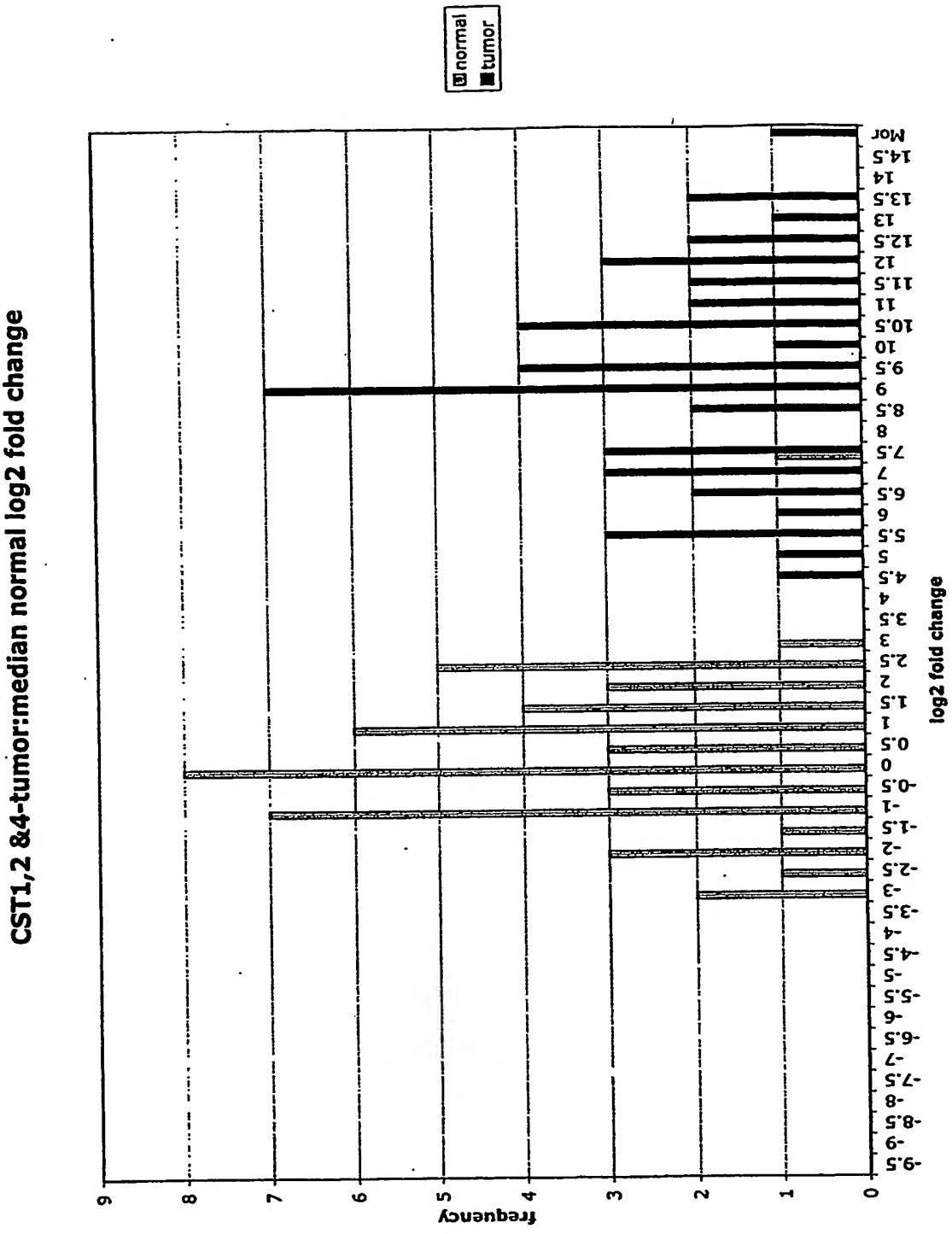
-8.5
-9
-9.5

Figure 5(a)


CST1,2 &4-tumor:median normal log2 fold change
normal
tumor
frequency
log2 fold change
0
1
2
3
4
5
6
7
8
9
-9.5
-9
-8.5
-8
-7.5
-7
-6.5
-6
-5.5
-5
-4.5
-4
-3.5
-3
-2.5
-2
-1.5
-1
-0.5
0
0.5
1
1.5
2
2.5
3
3.5
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4.5
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5.5
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6.5
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7.5
8
8.5
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11.5
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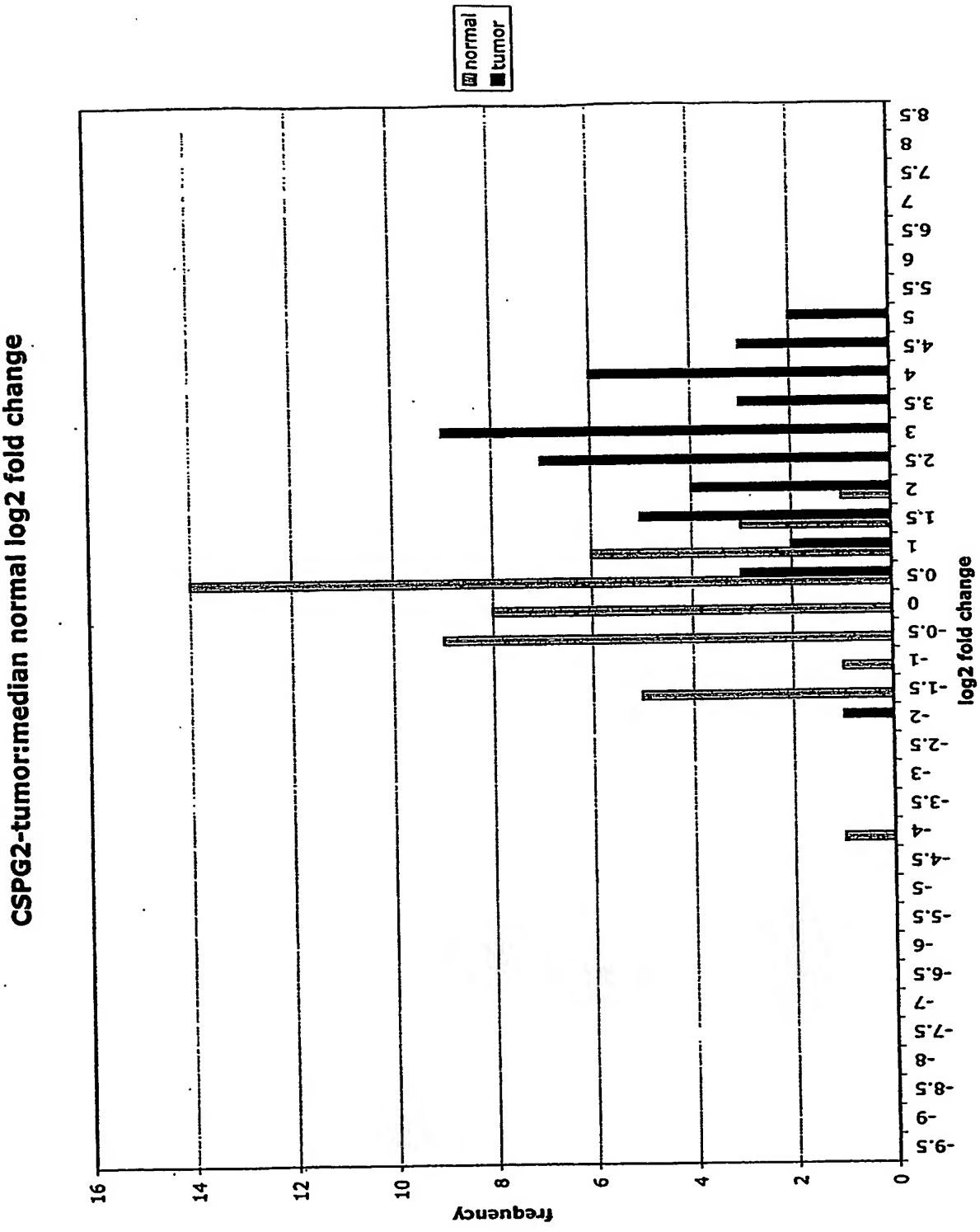
12.5
13
13.5
14
14.5
More

Figure 5(b)


CSPG2-tumor:median normal log2 fold change
normal
tumor
frequency
log2 fold change
16
14
12
10
8
6
4
2
0
8.5
8
7.5
7
6.5
6
5.5
5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
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-4
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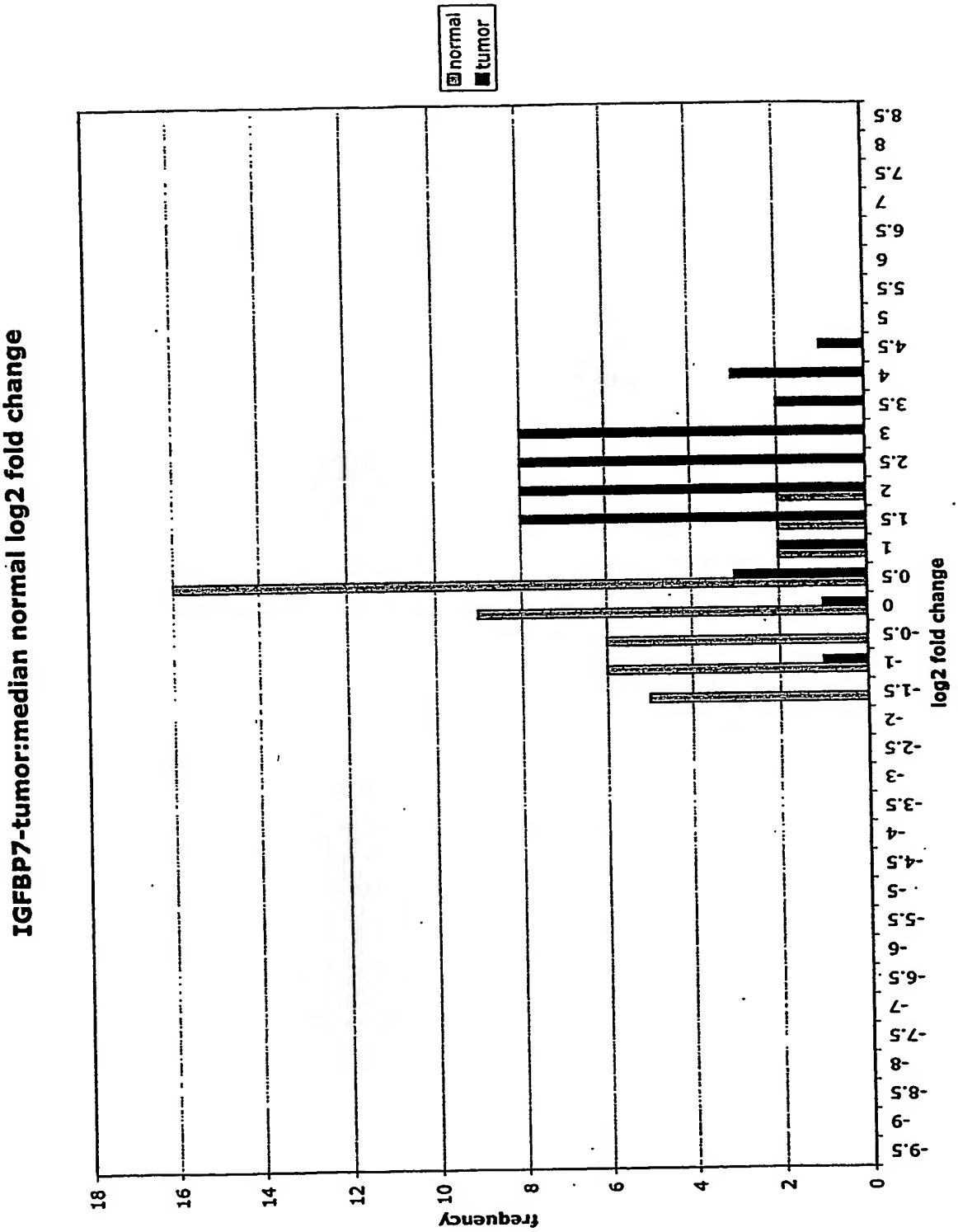
-8
-8.5
-9
-9.5

Figure 5(c)


IGFBP7-tumor:median normal log2 fold change
normal
tumor
frequency
log2 fold change
18
16
14
12
10
8
6
4
2
0
8.5
8
7.5
7
6.5
6
5.5
5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
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-2
-2.5
-3
-3.5
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-8.5
-9
-9.5

Figure 5(d)

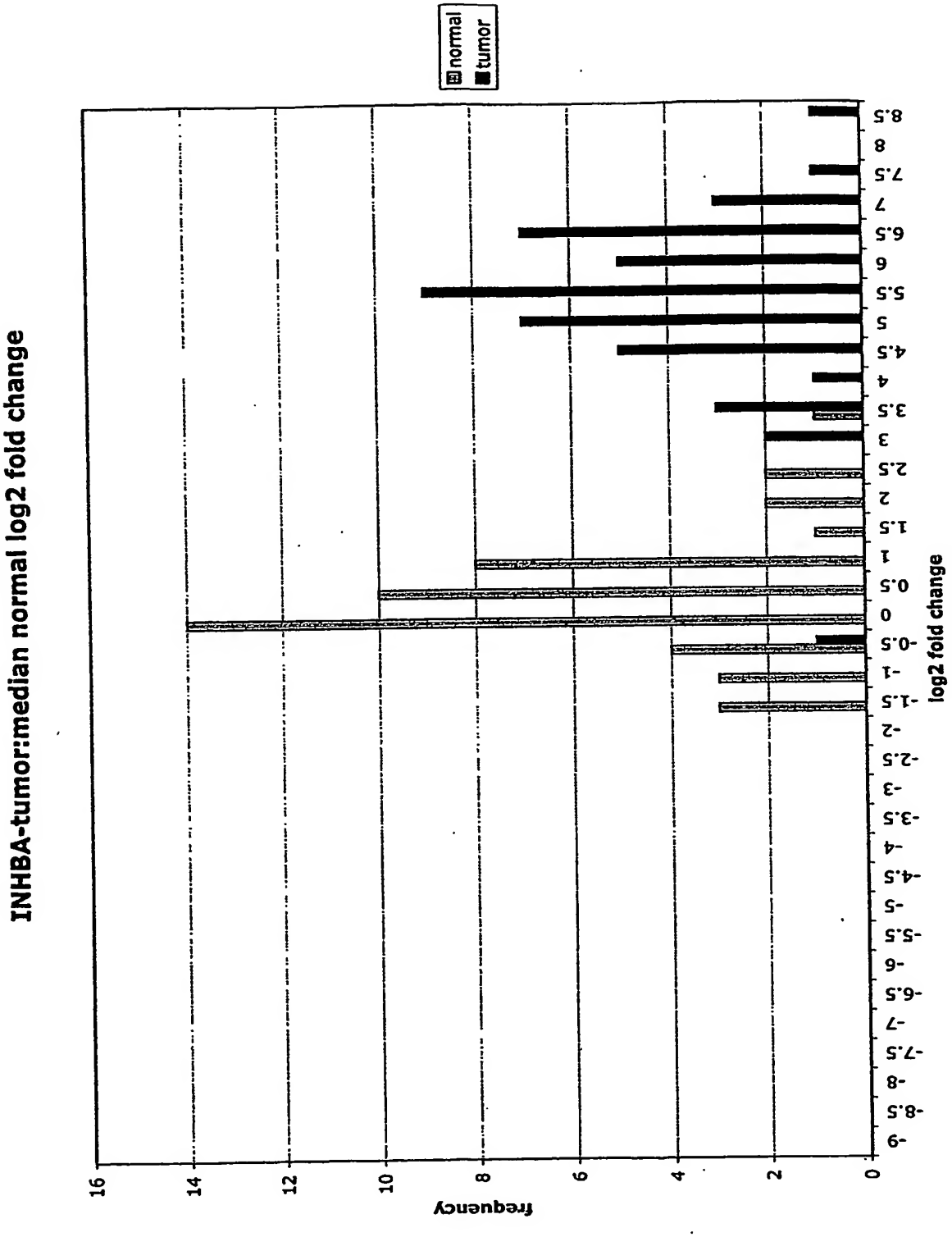
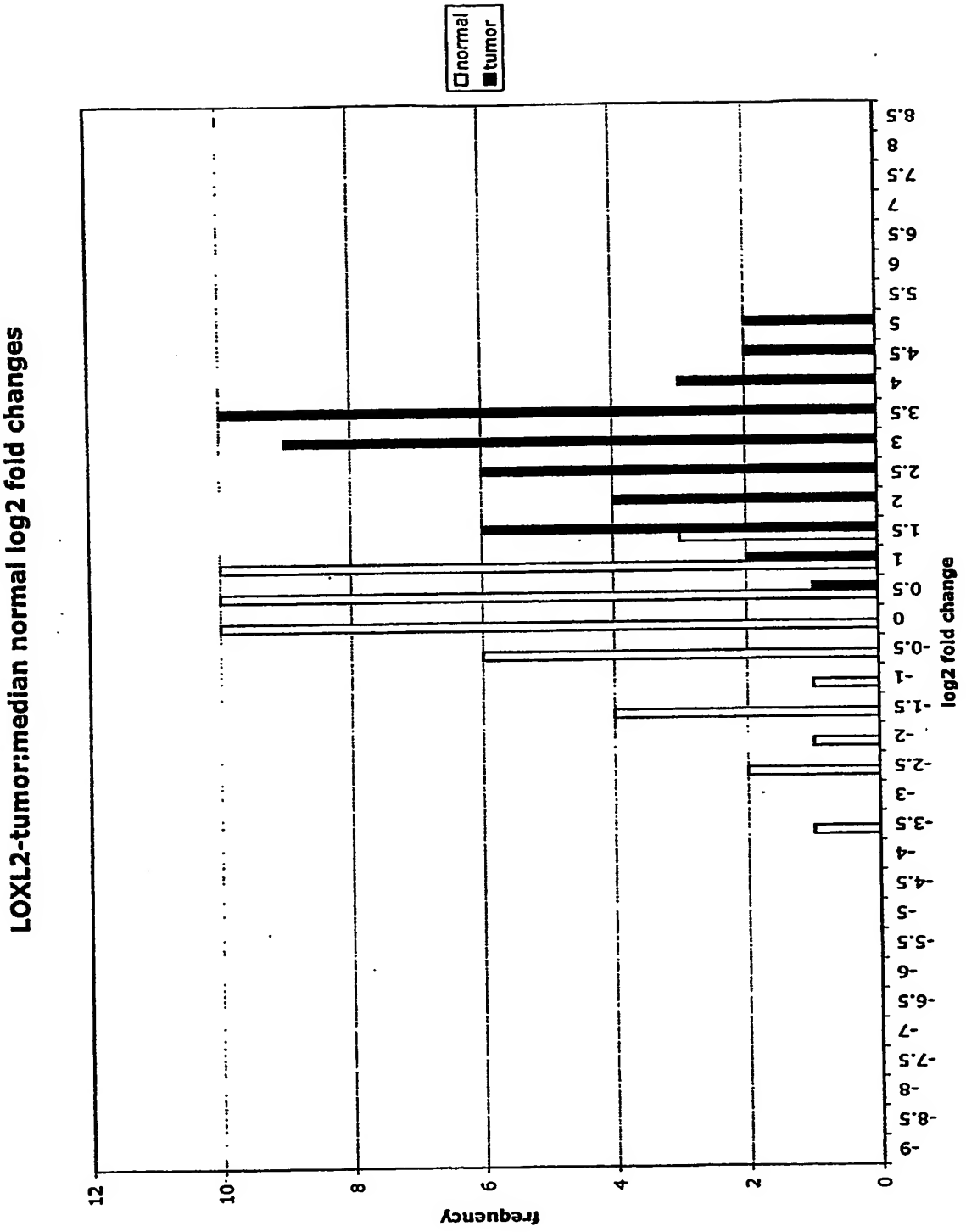

INHBA-tumor:median normal log2 fold change
normal
tumor
frequency
log2 fold change

Figure 5(e)


LOXL2-tumor:median normal log2 fold changes
normal
tumor
frequency
log2 fold change
12
10
8
6
4
2
0
8.5
8
7.5
7
6.5
6
5.5
5
4.5
4
3.5
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-0.5
-1
-1.5
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-2.5
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-3.5
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-8
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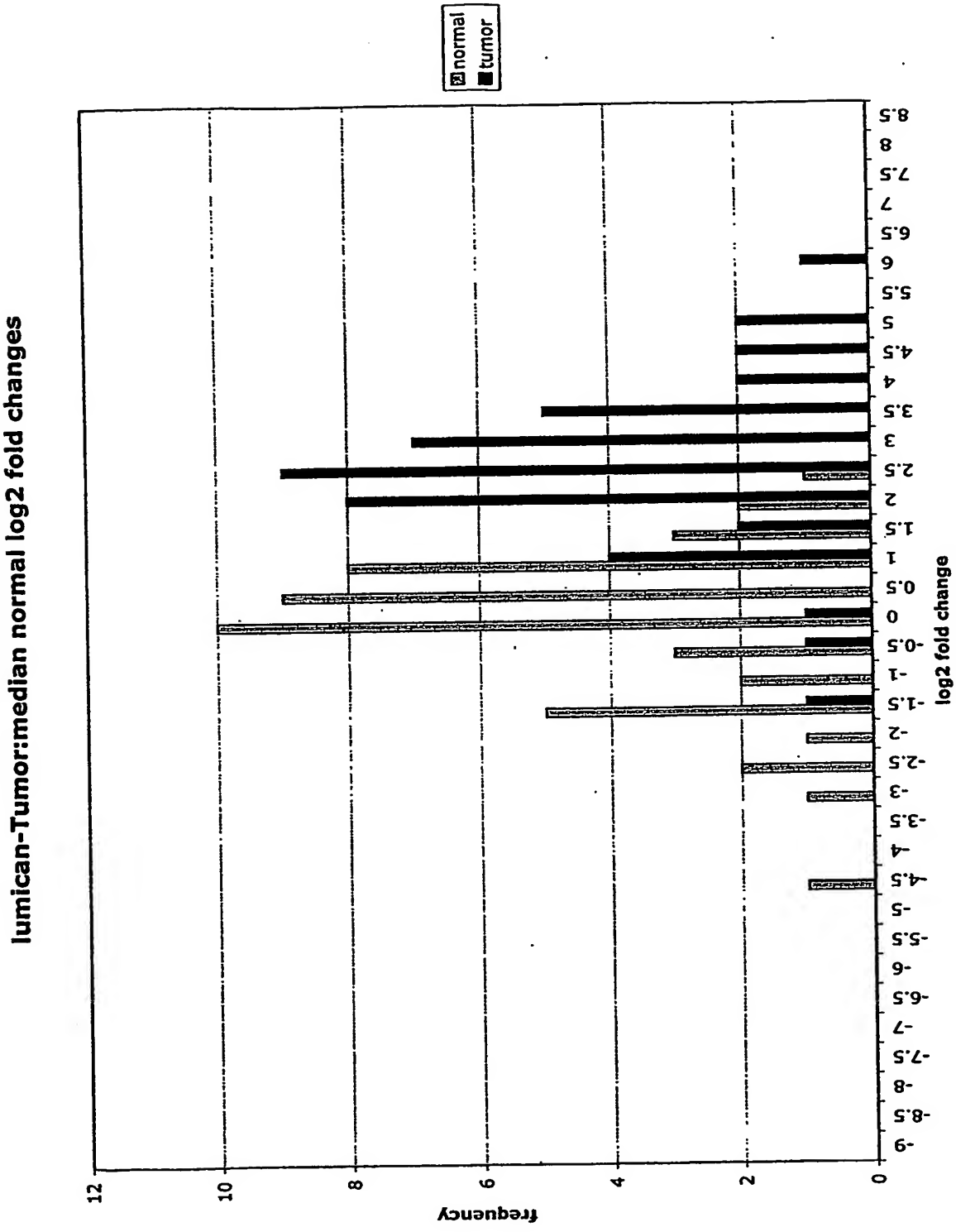
-9

Figure 5(f)


lumican-Tumor:median normal log2 fold changes
normal
tumor
frequency
log2 fold change
12
10
8
6
4
2
0
8.5
8
7.5
7
6.5
6
5.5
5
4.5
4
3.5
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-2
-2.5
-3
-3.5
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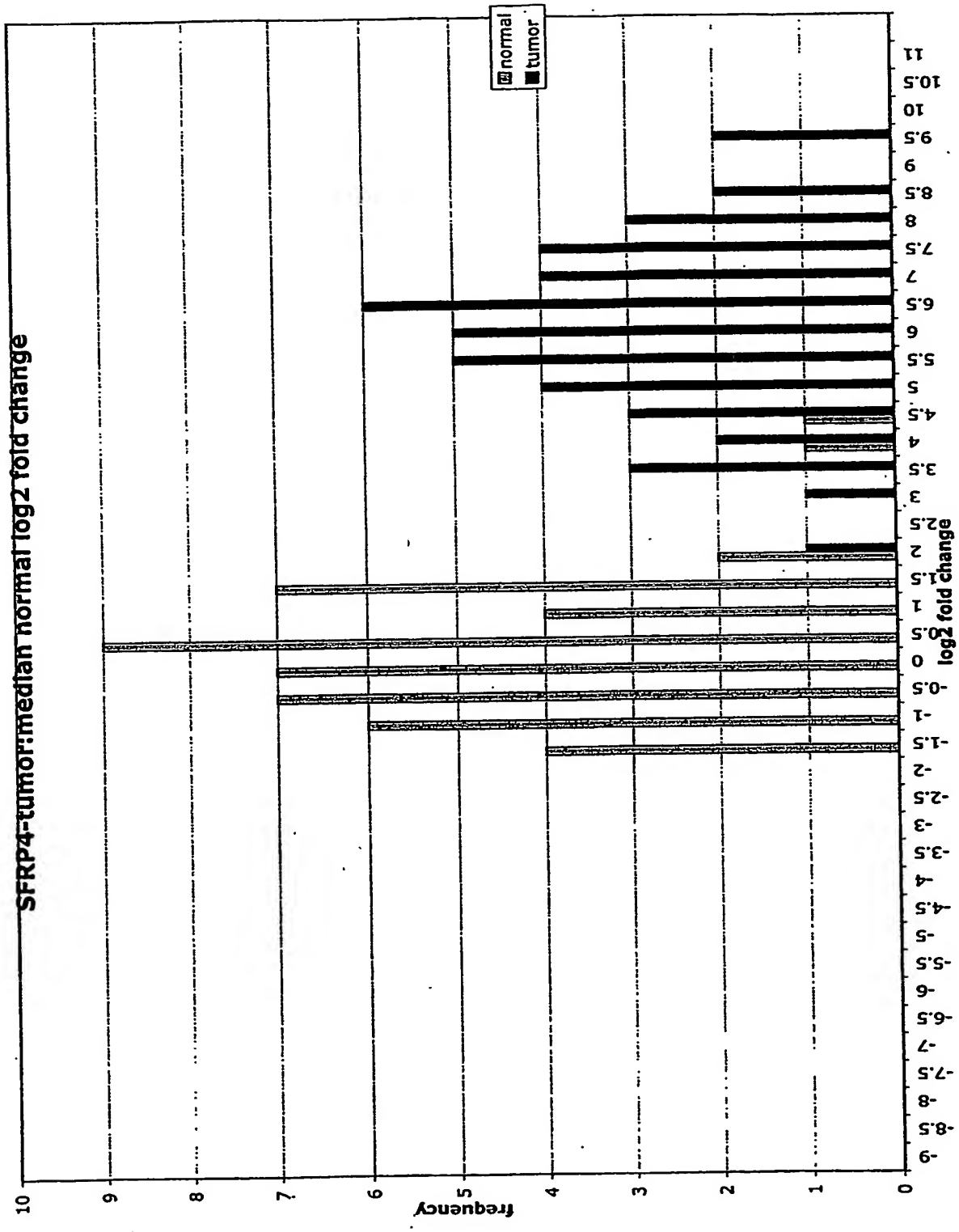
-8.5
-9

Figure 5(g)


SFRP4-tumor:median normal log2 fold change
normal
tumor
frequency
log2 fold change
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11
10.5
10
9.5
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8
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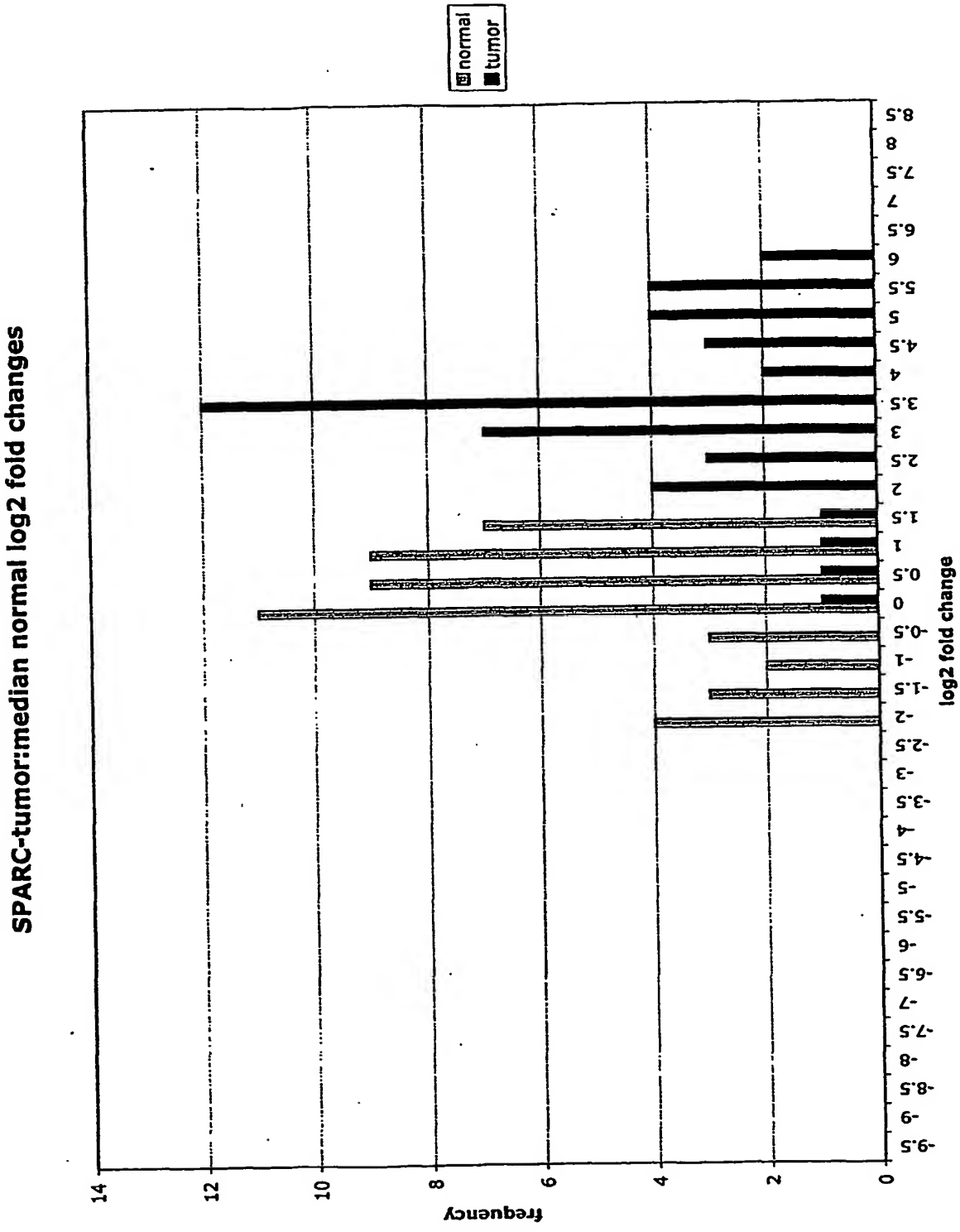
-9

Figure 5(h)


SPARC-tumor:median normal log2 fold changes
normal
tumor
frequency
log2 fold change
14
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-9
-9.5

Figure 5(i)

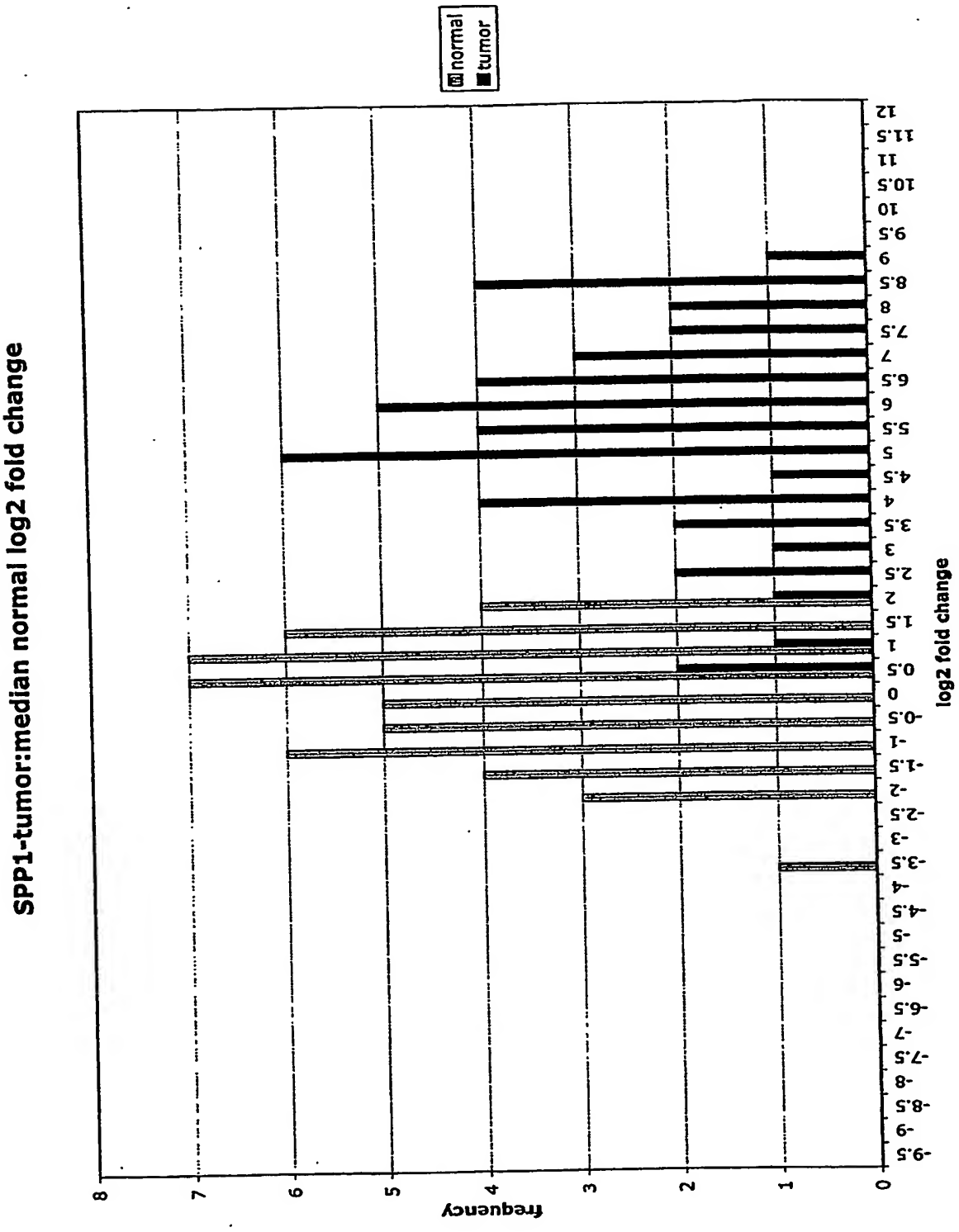

SPP1-tumor:median normal log2 fold change
normal
tumor
frequency
log2 fold change

Figure 5(j)

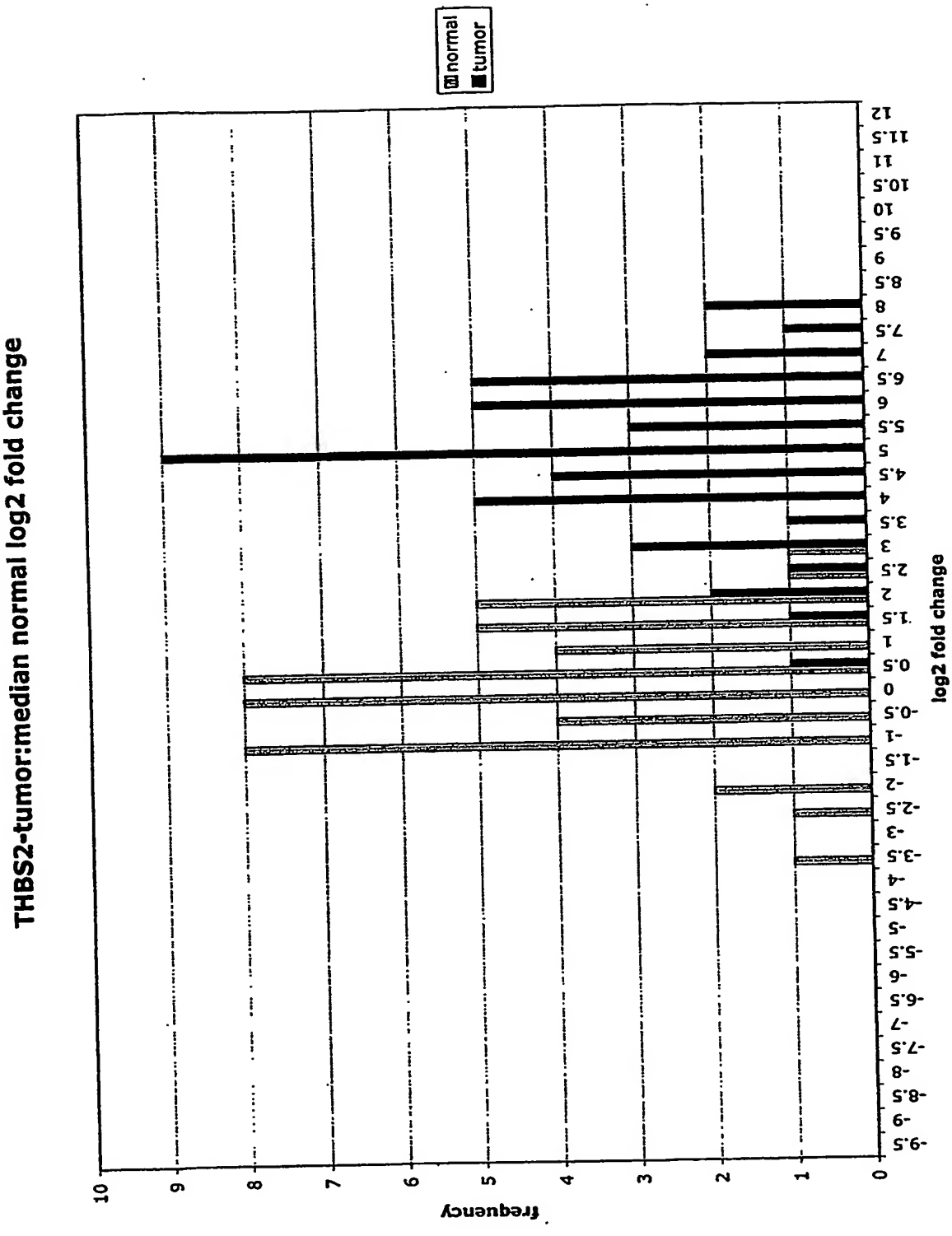

THBS2-tumor:median normal log2 fold change
normal
tumor
frequency
log2 fold change

Figure 5(k)

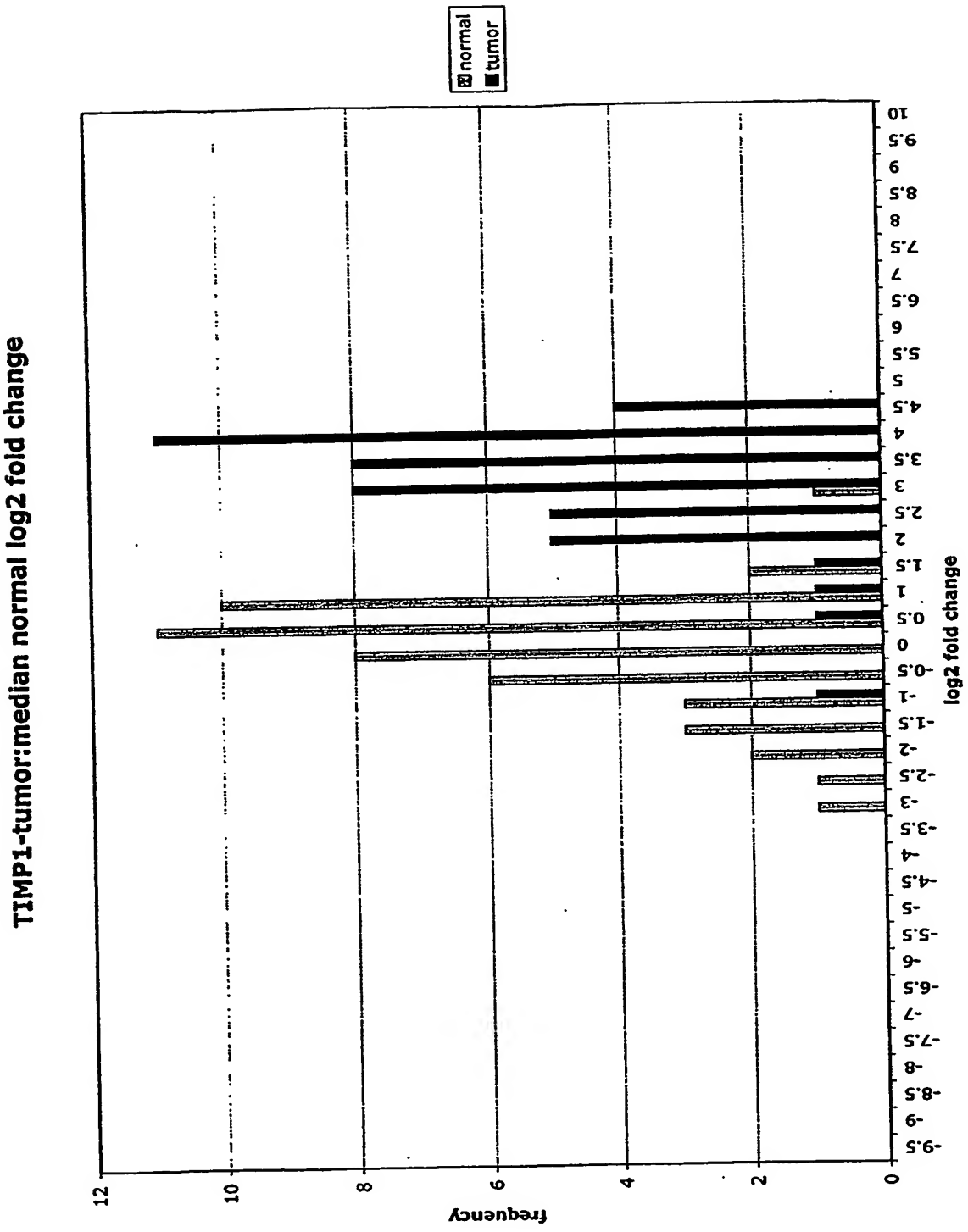

TIMP1-tumor:median normal log2 fold change
normal
tumor
frequency
log2 fold change
12
10
8
6
4
2
0
10
9.5
9
8.5
8
7.5
7
6.5
6
5.5
5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
-2.5
-3
-3.5
-4
-4.5
-5
-5.5
-6
-6.5
-7
-7.5
-8
-8.5
-9
-9.5

Figure 5(l)

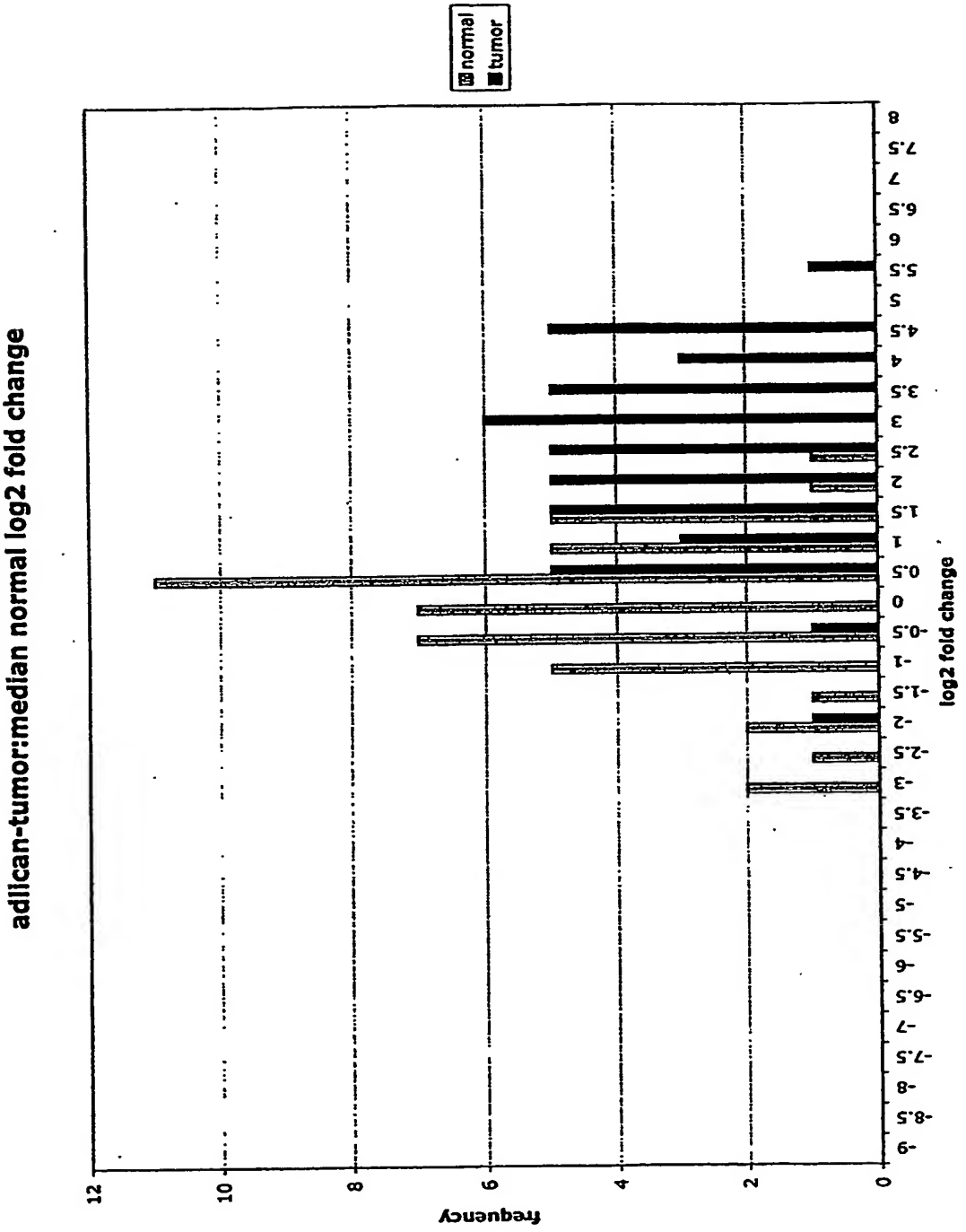

adlican-tumor:median normal log2 fold change
normal
tumor
frequency
log2 fold change

Figure 5(m)

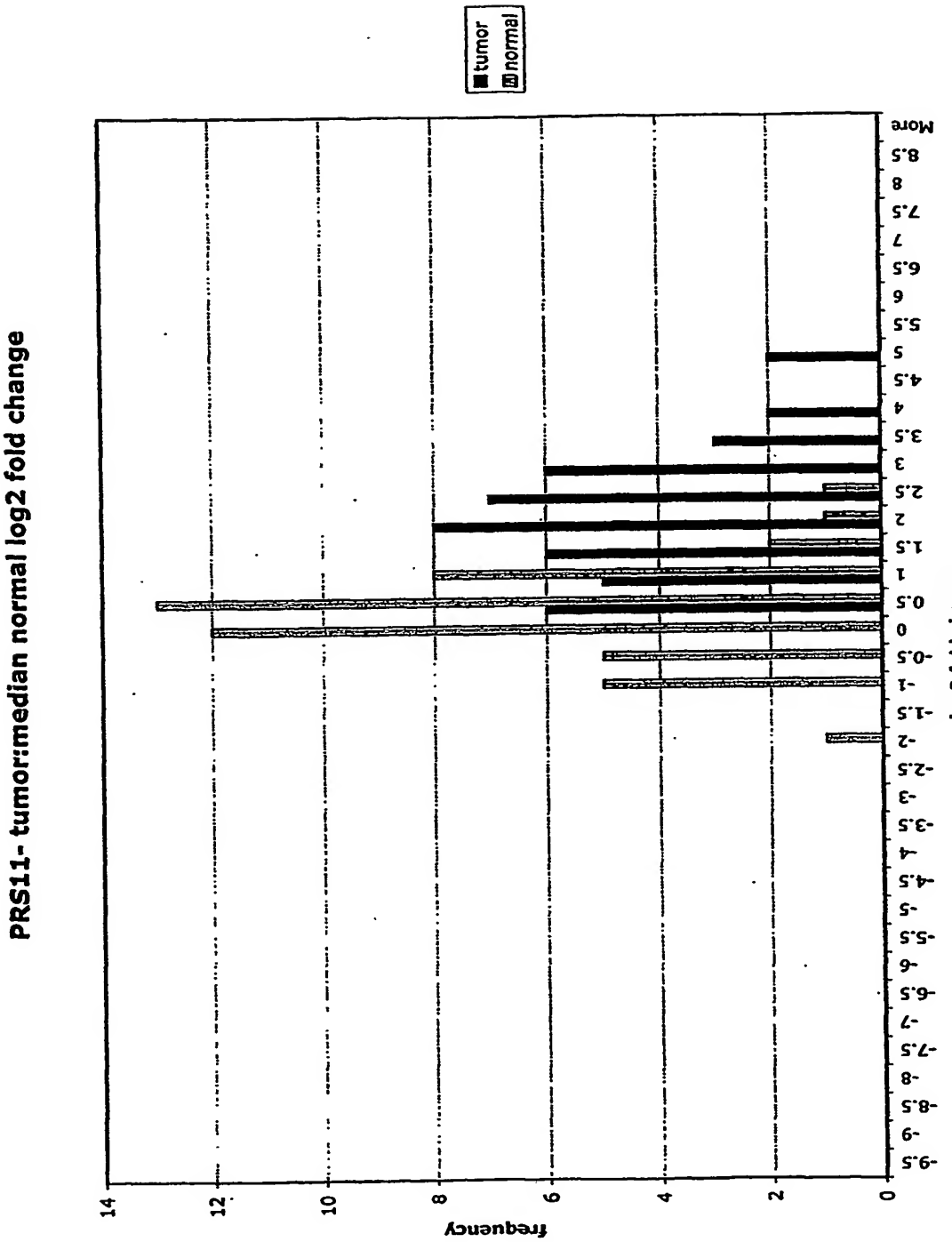

PRS11- tumor:median normal log2 fold change
tumor
normal
frequency
log2 fold change
14
12
10
8
6
4
2
0
More
8.5
8
7.5
7
6.5
6
5.5
5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
-2.5
-3
-3.5
-4
-4.5
-5
-5.5
-6
-6.5
-7
-7.5
-8
-8.5
-9
-9.5

Figure 5(n)

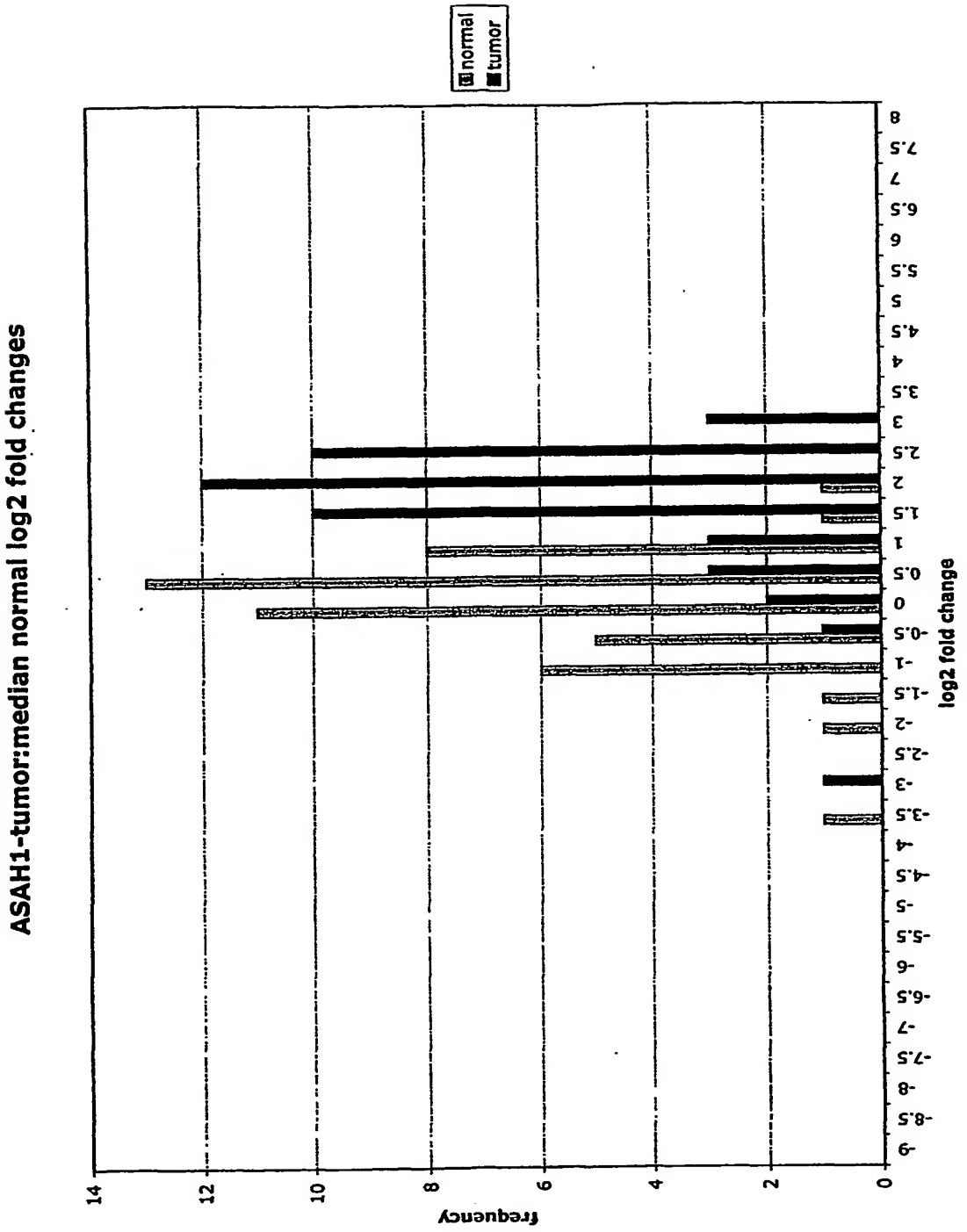

ASAH1-tumor:median normal log2 fold changes
normal
tumor
frequency
log2 fold change

Figure 5(o)

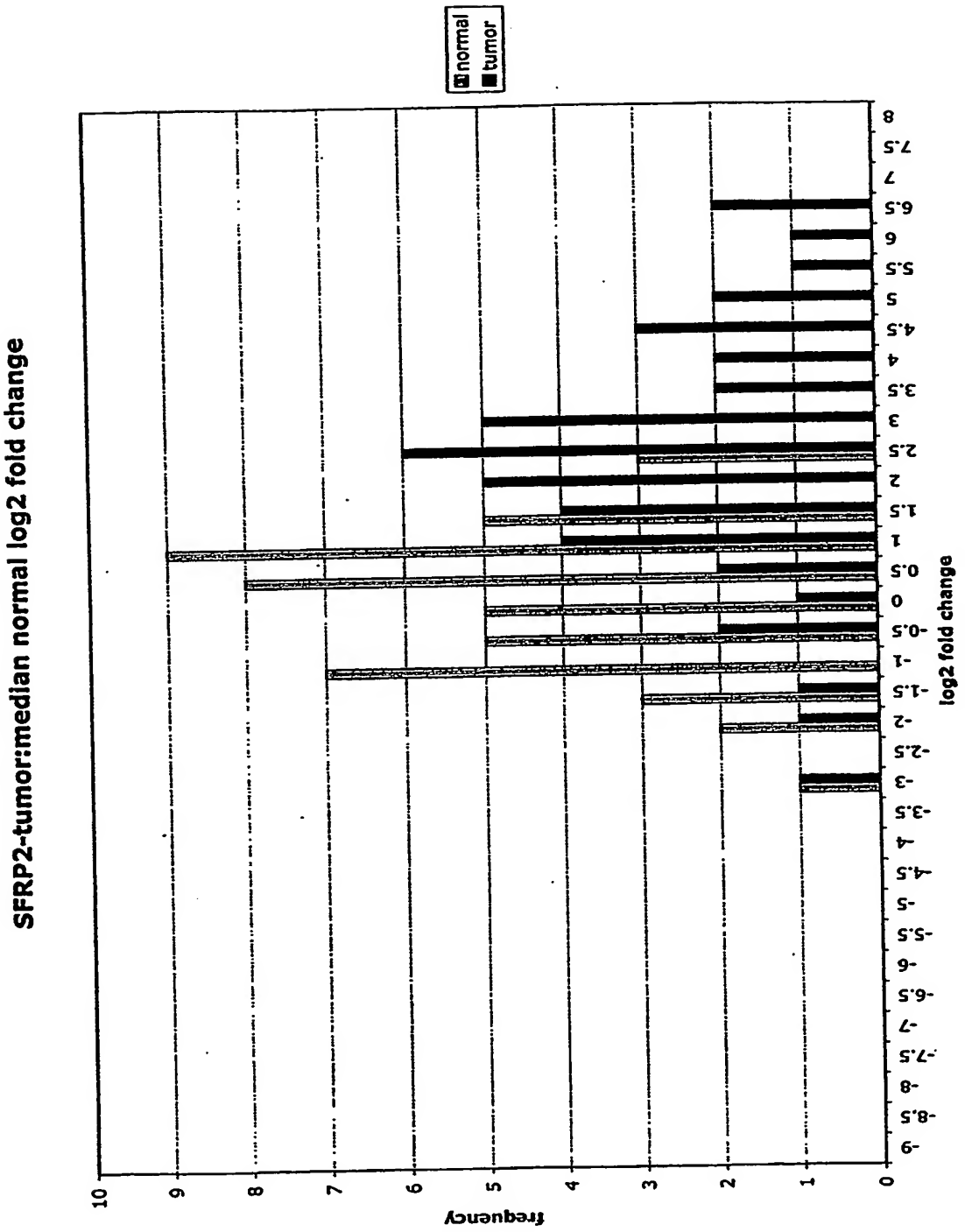

SFRP2-tumor:median normal log2 fold change
normal
tumor
frequency
log2 fold change

Figure 5(p)

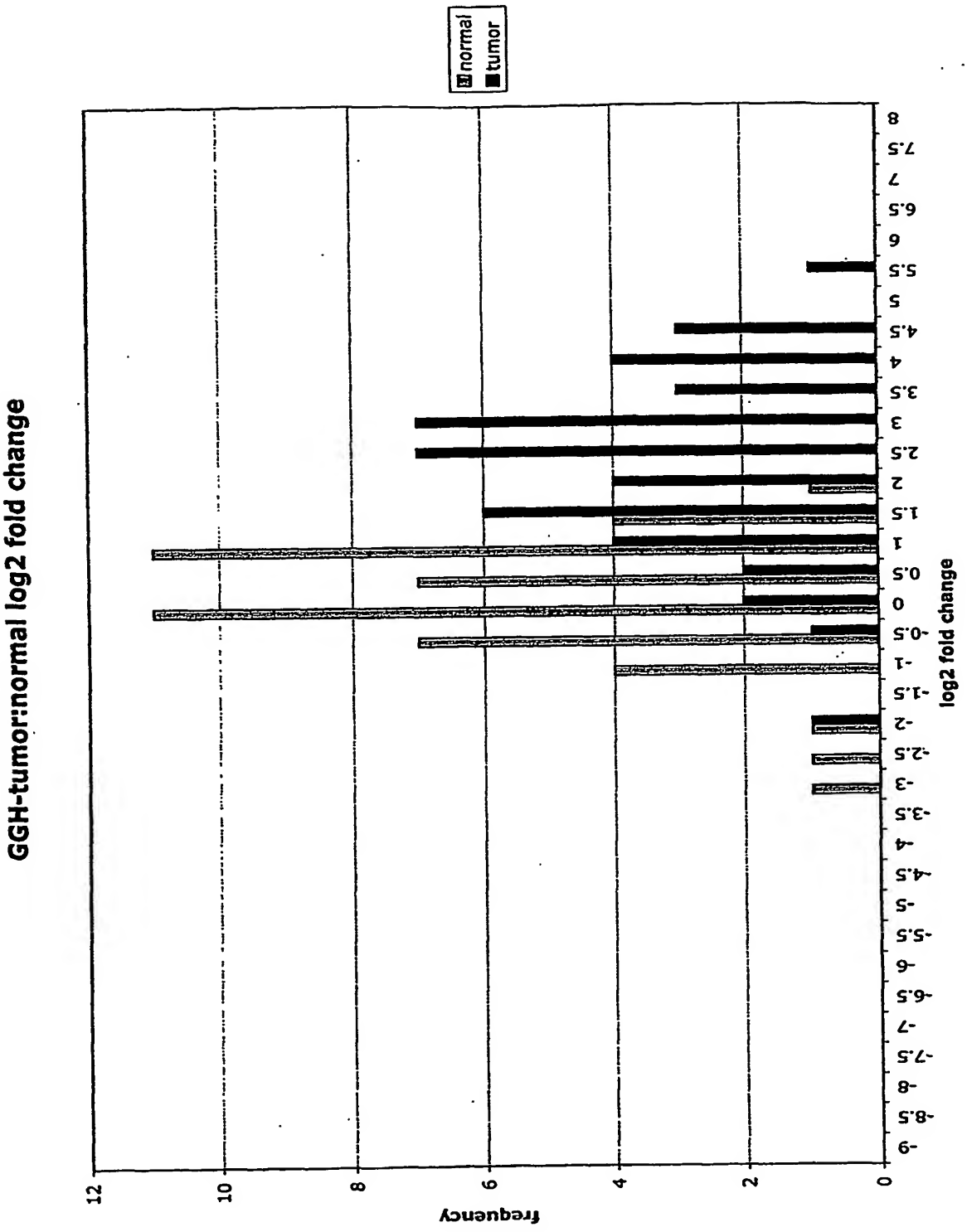

GGH-tumor:normal log2 fold change
normal
tumor
frequency
log2 fold change
12
10
8
6
4
2
0
8
7.5
7
6.5
6
5.5
5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
-2.5
-3
-3.5
-4
-4.5
-5
-5.5
-6
-6.5
-7
-7.5
-8
-8.5
-9

Figure 5(q)

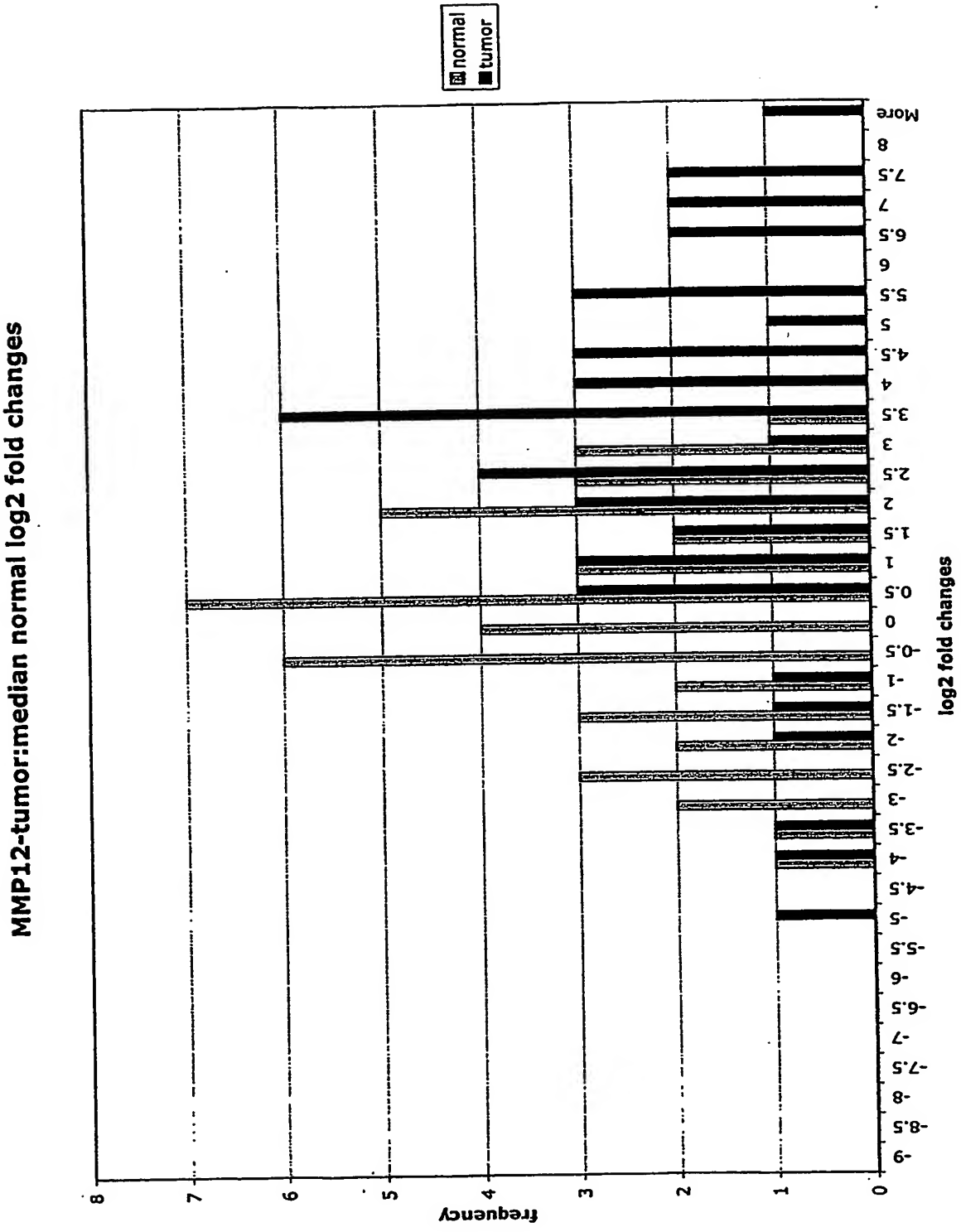

MMP12-tumor:median normal log2 fold changes
normal
tumor
frequency
log2 fold changes
0
1
2
3
4
5
6
7
8
-9
-8.5
-8
-7.5
-7
-6.5
-6
-5.5
-5
-4.5
-4
-3.5
-3
-2.5
-2
-1.5
-1
-0.5
0
0.5
1
1.5
2
2.5
3
3.5
4
4.5
5
5.5
6
6.5
7
7.5
8
More

Figure 5(r)

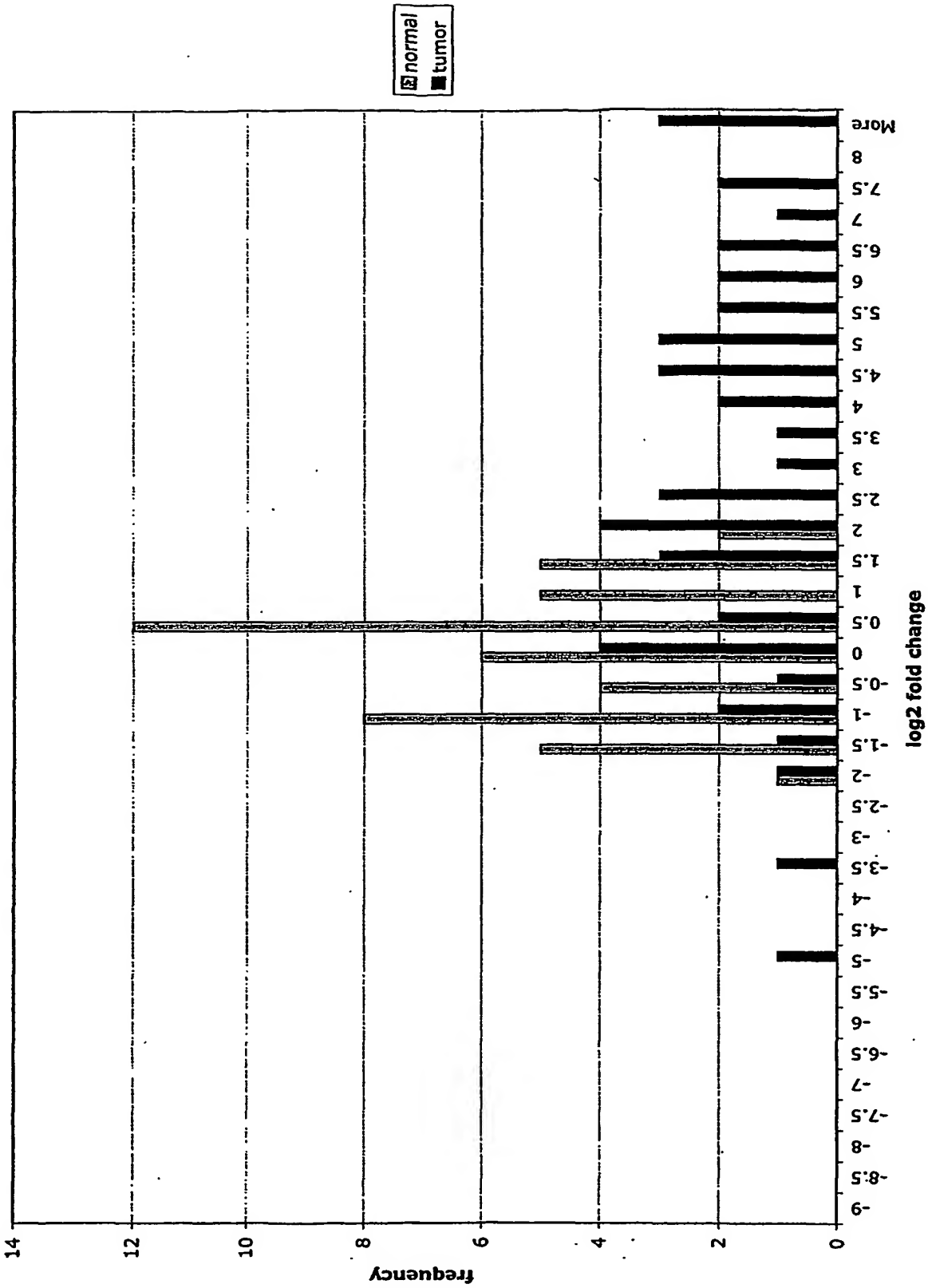

normal
tumor
frequency
0
2
4
6
8
10
12
14
log2 fold change
More
8
7.5
7
6.5
6
5.5
5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
-2.5
-3
-3.5
-4
-4.5
-5
-5.5
-6
-6.5
-7
-7.5
-8
-8.5
-9

Figure 5(s)

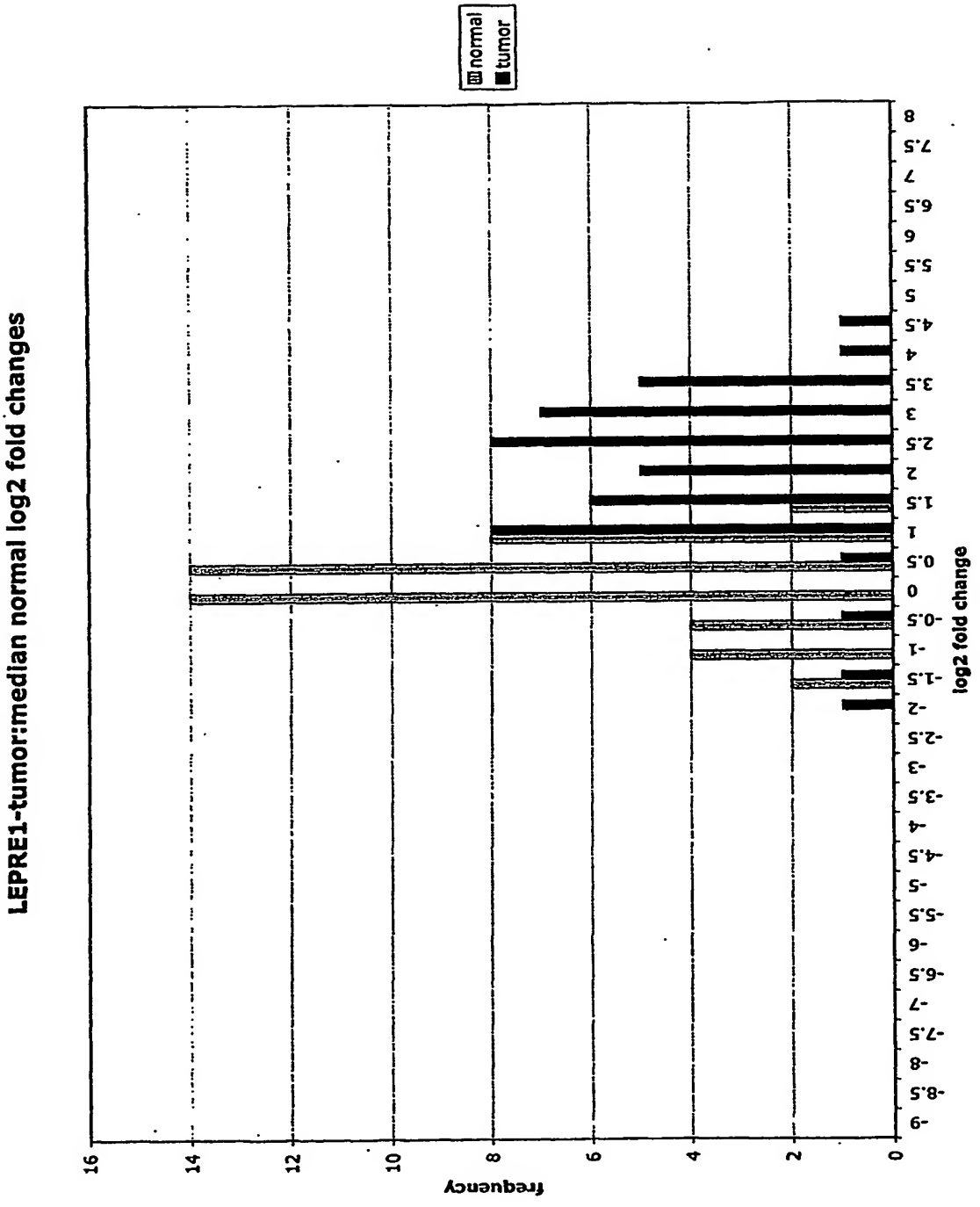

LEPRE1-tumor:median normal log2 fold changes
normal
tumor
frequency
log2 fold change

Figure 5(t)

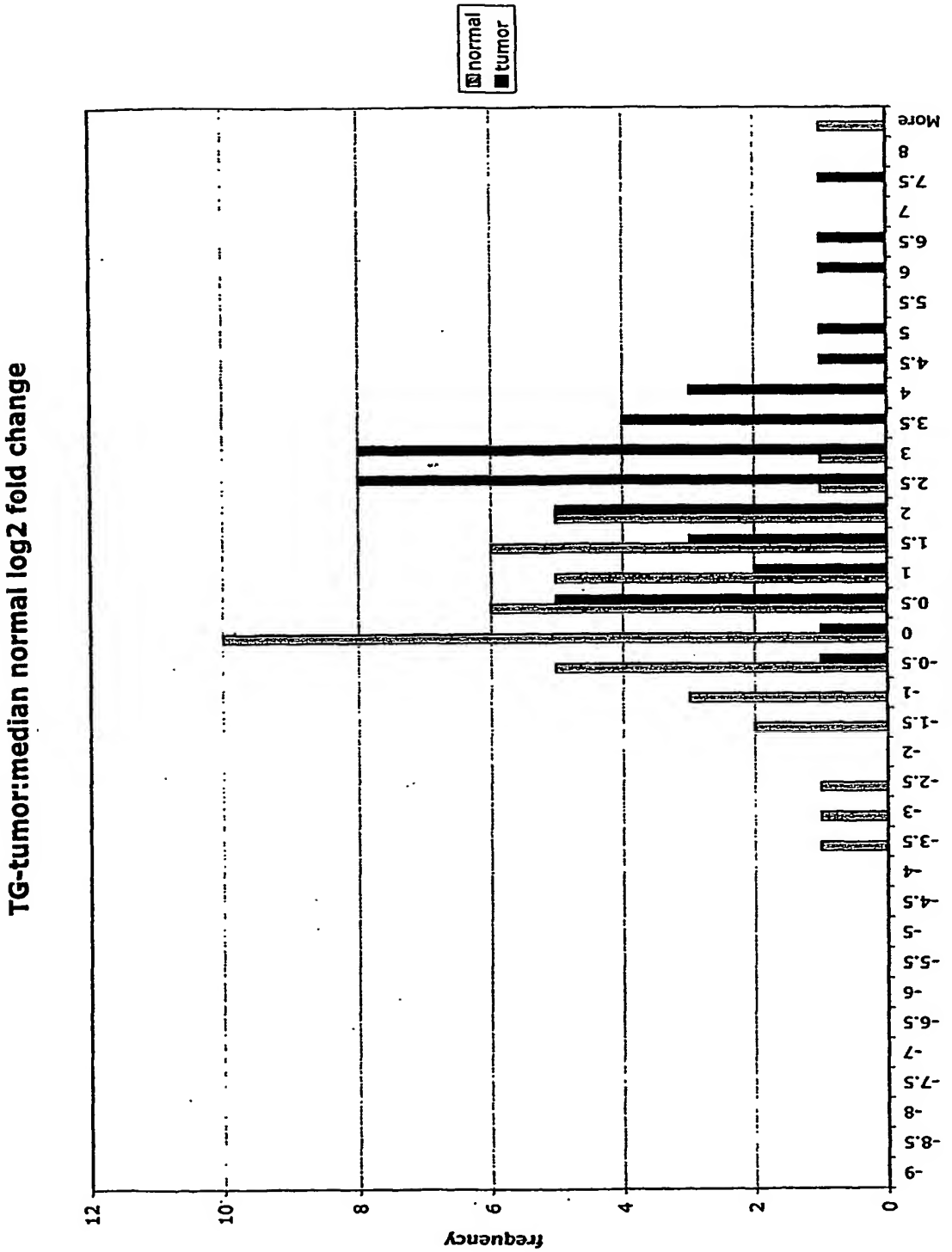

TG-tumor:median normal log2 fold change
normal
tumor
frequency
log2 fold change
12
10
8
6
4
2
0
-9
-8.5
-8
-7.5
-7
-6.5
-6
-5.5
-5
-4.5
-4
-3.5
-3
-2.5
-2
-1.5
-1
-0.5
0
0.5
1
1.5
2
2.5
3
3.5
4
4.5
5
5.5
6
6.5
7
7.5
8
More

Figure 5(u)

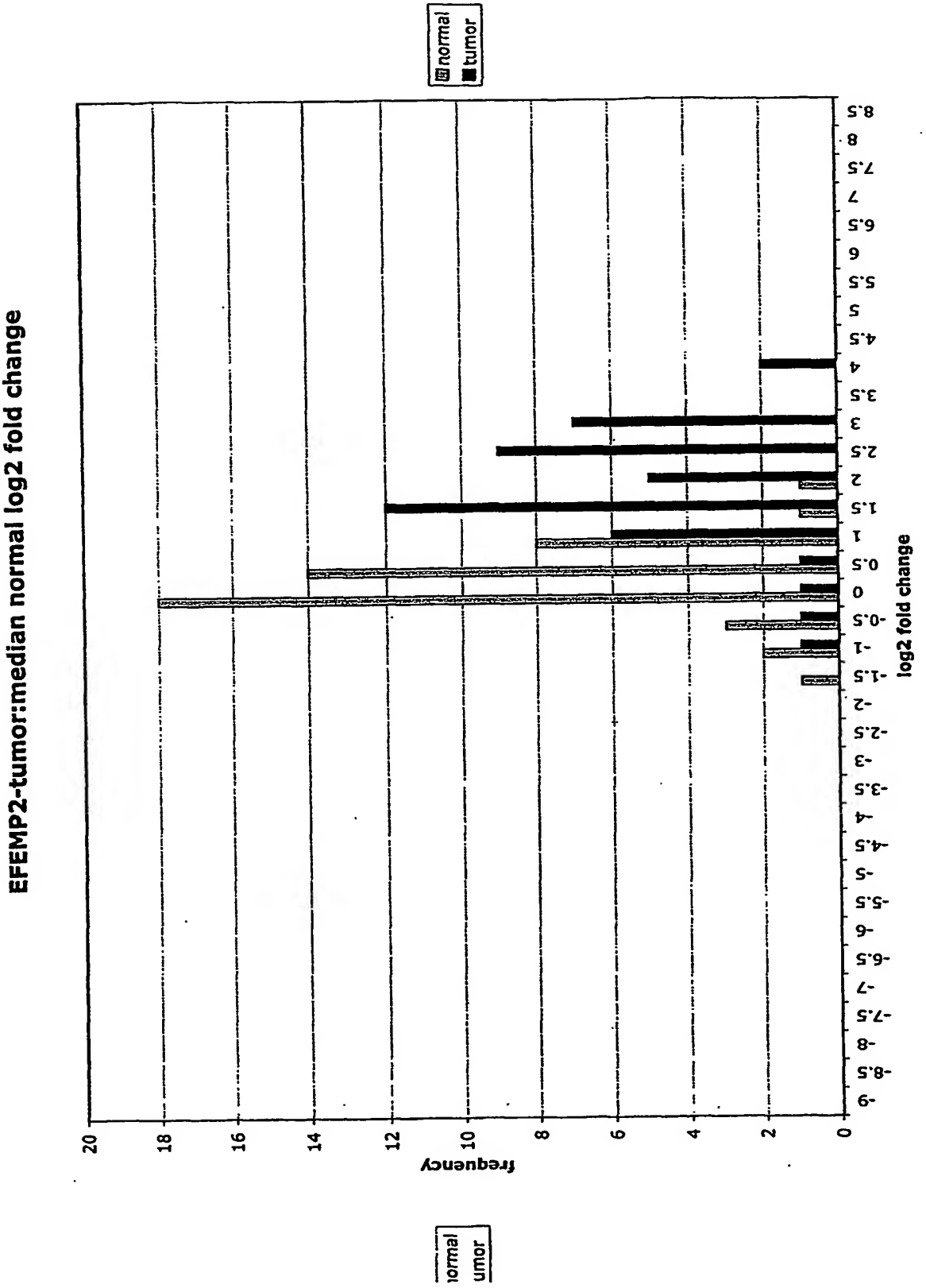

EFEMP2-tumor:median normal log2 fold change
normal
tumor
frequency
log2 fold change

Figure 5(v)

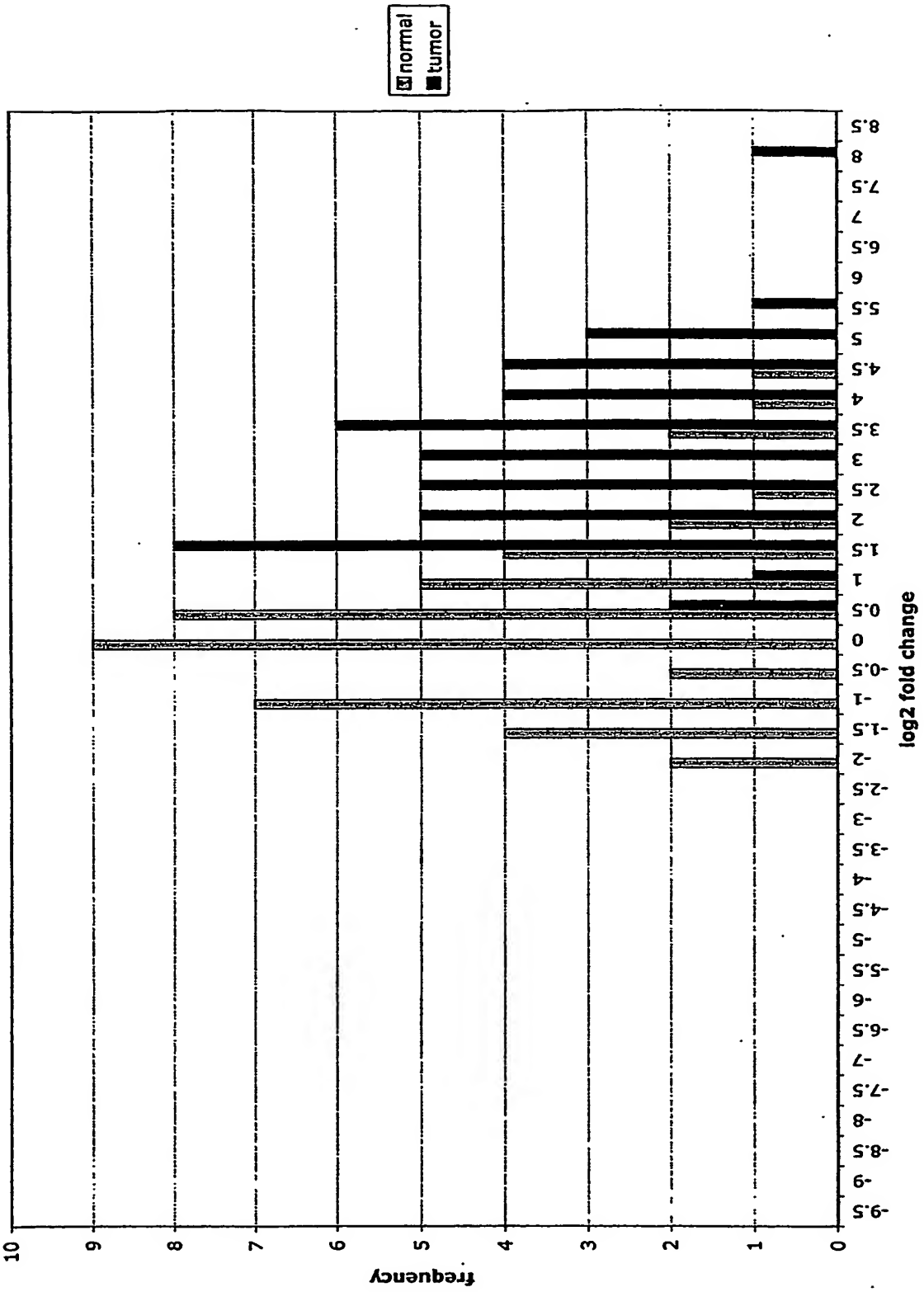

normal
tumor
frequency
log2 fold change
10
9
8
7
6
5
4
3
2
1
0
8.5
8
7.5
7
6.5
6
5.5
5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
-2.5
-3
-3.5
-4
-4.5
-5
-5.5
-6
-6.5
-7
-7.5
-8
-8.5
-9
-9.5

Figure 5(w)

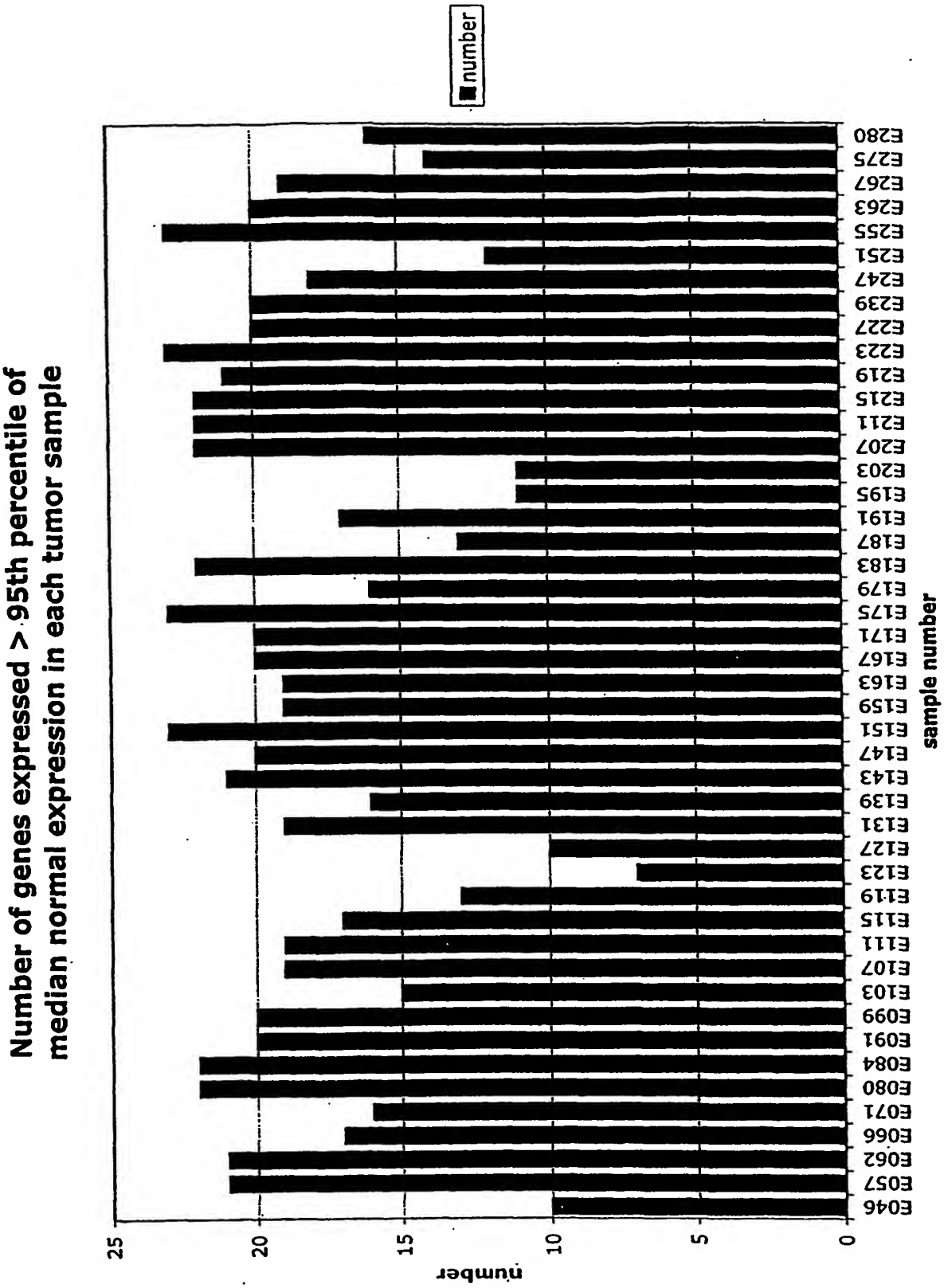
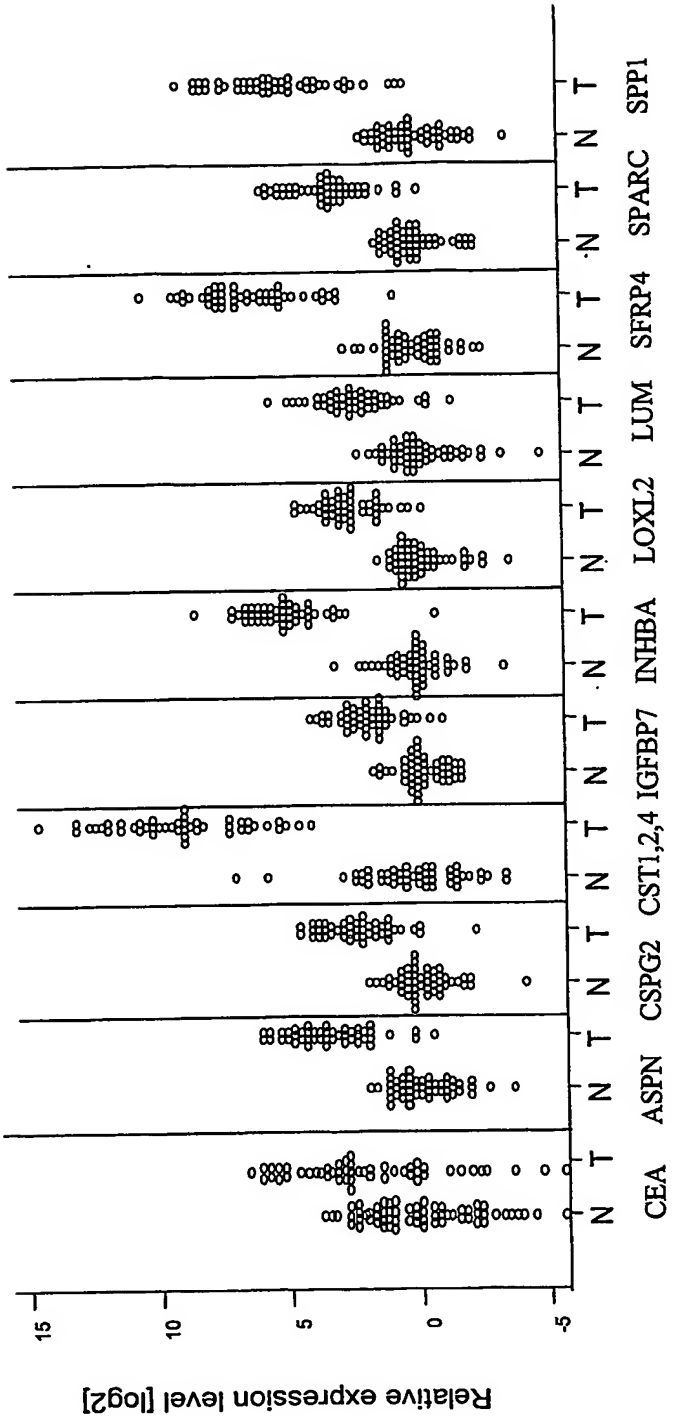

Number of genes expressed > 95th percentile of median normal expression in each tumor sample
number
25
20
15
10
5
0
E046
E057
E062
E066
E071
E080
E084
E091
E099
E103
E107
E111
E115
E119
E123
E127
E131
E139
E143
E147
E151
E159
E163
E167
E171
E175
E179
E183
E187
E191
E195
E203
E207
E211
E215
E219
E223
E227
E239
E247
E251
E255
E263
E267
E275
E280
sample number

Figure 6

Fig.7a Relative expression of markers in tumor and normal samples compared to CEA



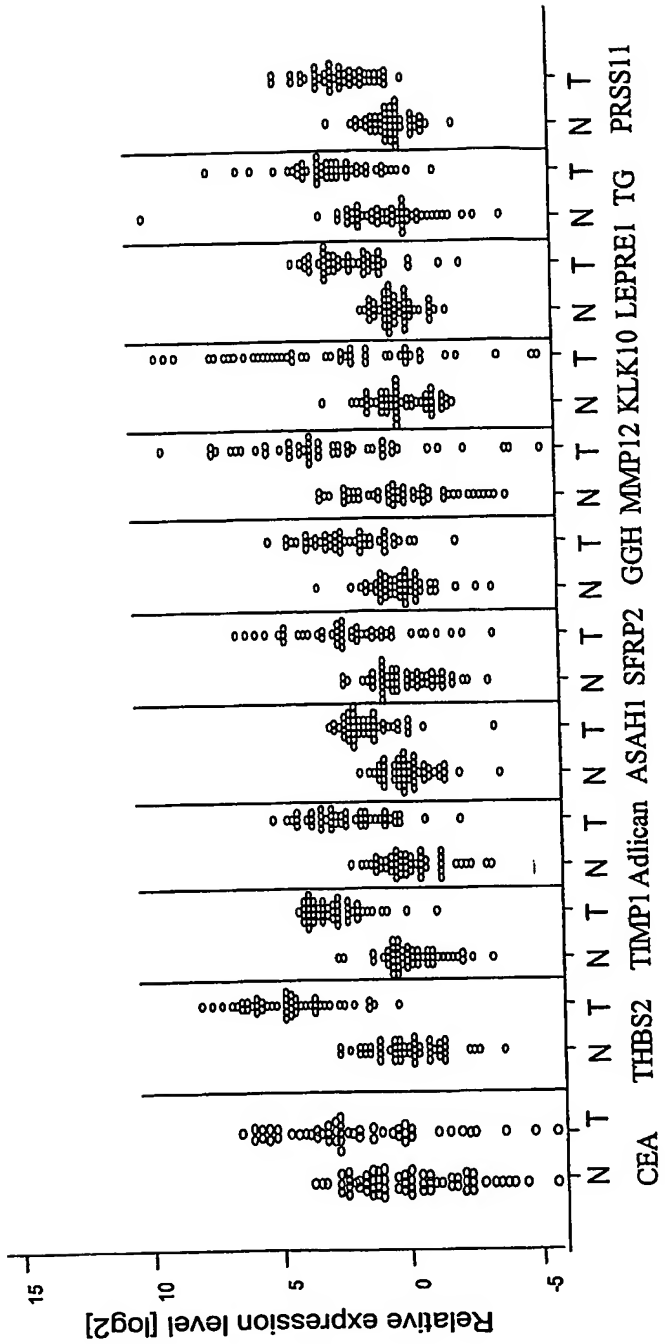

Relative expression level [log2]
15
10
5
0
-5
N T N T N T N T N T N T N T N T N T N T N T N T N T
CEA THBS2 TIMP1 Adlican ASAH1 SFRP2 GGH MMP12 KLK10 LEPRE1 TG PRSS11

Fig. 7b

Fig. 7c

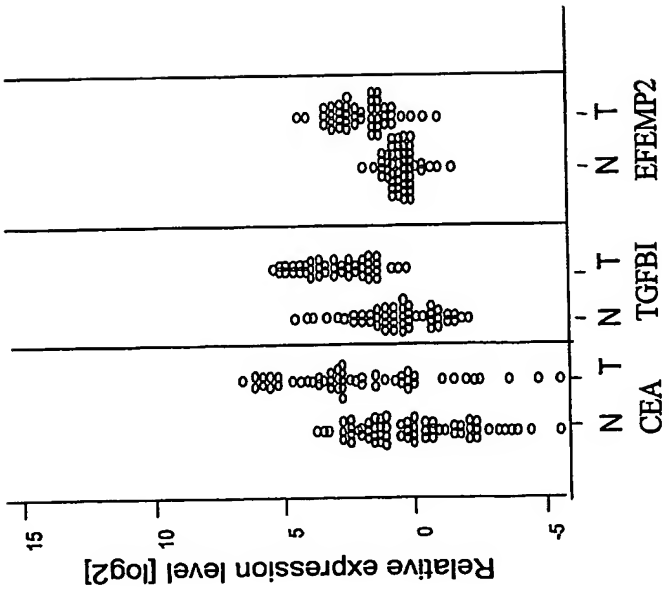
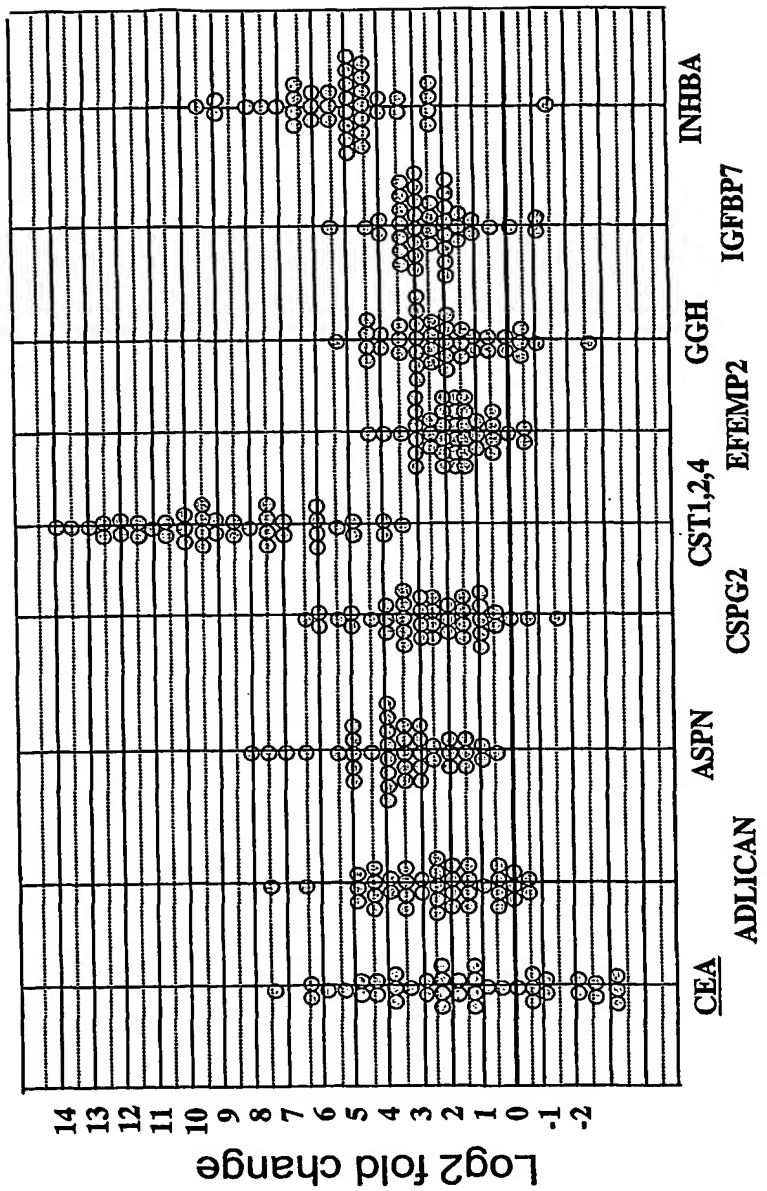

Relative expression level [log2]
15
10
5
0
-5
N T N T N T
CEA TGFBI EFEMP2

Fig. 8. Quantitative RT-PCR: expression in paired tumor and non-malignant samples of selected gastric cancer markers

name	symbol	median T:N fold change	maximum T:N fold change	% tumor samples with expression >paired non-malignant sample
adlican		5	146	88
asporin (lrr class 1)	ASPN	11	198	100
chondroitin sulfate proteoglycan 2 (versican)	CSPG2	5	68	93
cystatins SN, SA & S	CST1, 2, 4	498	11911	100
egf-containing fibulin-like extracellular matrix protein 2	EFEMP2	3	17	93
gamma-glutamyl hydrolase	GGH	4	34	83
inhibin beta A chain	INHBA	27	630	95
insulin-like growth factor binding protein 7	IGFBP7	5	38	93
kallikrein 10	KLK10	7	519	78
leucine proline-enriched proteoglycan 1(leprecan 1)	LEPRE1	4	23	85
lumican	LUM	5	68	90
lysyl oxidase-like 2	LOXL2	7	53	95
matrix metalloproteinase 12	MMP12	9	468	85
metalloproteinase inhibitor 1	TIMP1	6	103	95
n-acylsphingosine amidohydrolase	ASAH1	3	15	88
osteopontin	SPP1	36	626	98
secreted frizzled-related protein 2	SFRP2	5	48	83
secreted frizzled-related protein 4	SFRP4	54	375	100
secreted protein, acidic, cysteine rich	SPARC	10	66	95
serine protease 11 (IGF binding)	PRSS11	4	63	90
thrombospondin 2	THBS2	23	452	98
thyroglobulin	TG	4	174	93
transforming growth factor B-induced	TGFBI	5	78	95
cell growth regulatory factor with EF-hand domain	CGR11	3	33	75
serine (or cysteine) proteinase inhibitor H1	SERPINH1	10	51	98
matrix metalloproteinase 12	MMP2	2	46	83
proprotein convertase subtilisin/kexin type 5	PCSK5	2	63	80
serine (or cysteine) proteinase inhibitor B5	SERPINB5	5	861	73
transforming growth factor β1	TGFB1	3	16	88
carcinoembryonic antigen (CEA)	CEACAM5	3	177	68

Fig. 9a Relative tumor:normal fold changes in paired tumor/normal gastric samples



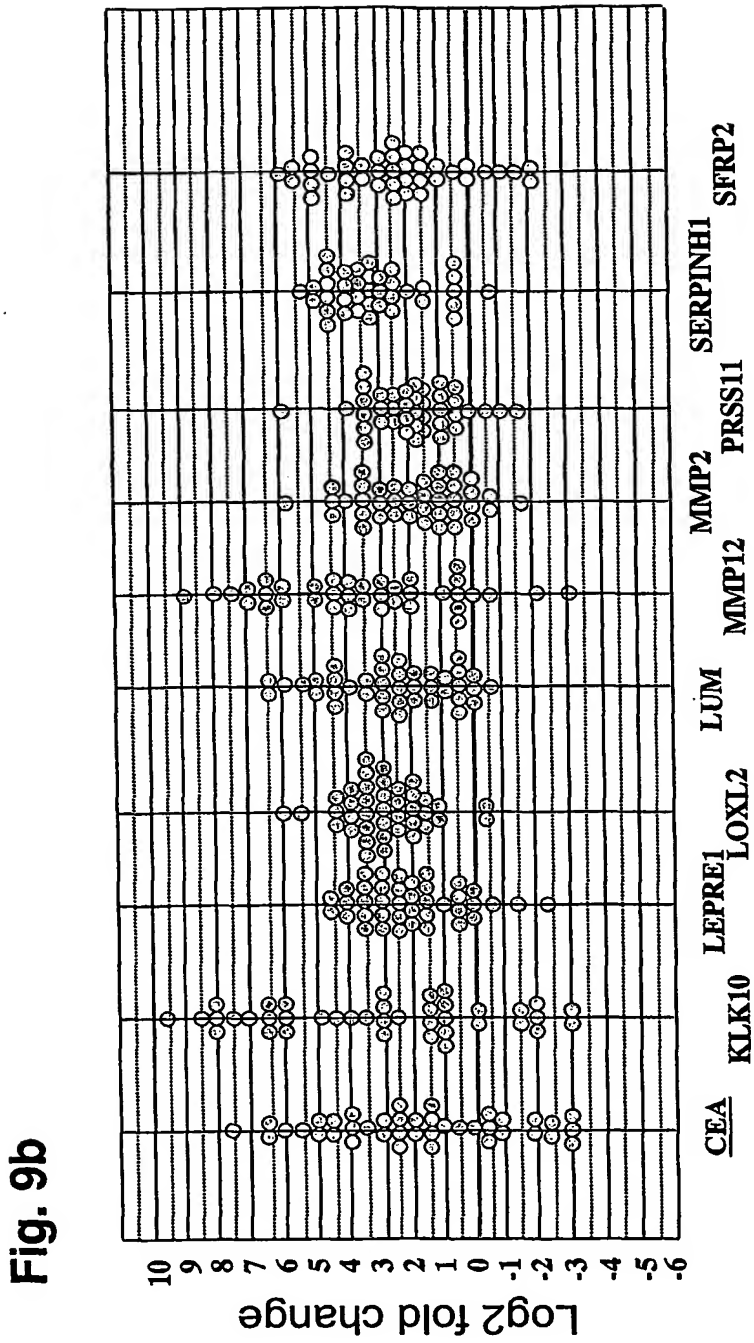

Log2 fold change
10
9
8
7
6
5
4
3
2
1
0
-1
-2
-3
-4
-5
-6
CEA
KLK10
LEPRE1
LOXL2
LUM
MMP12
MMP2
PRSS11
SERPINH1
SFRP2

Fig. 9b

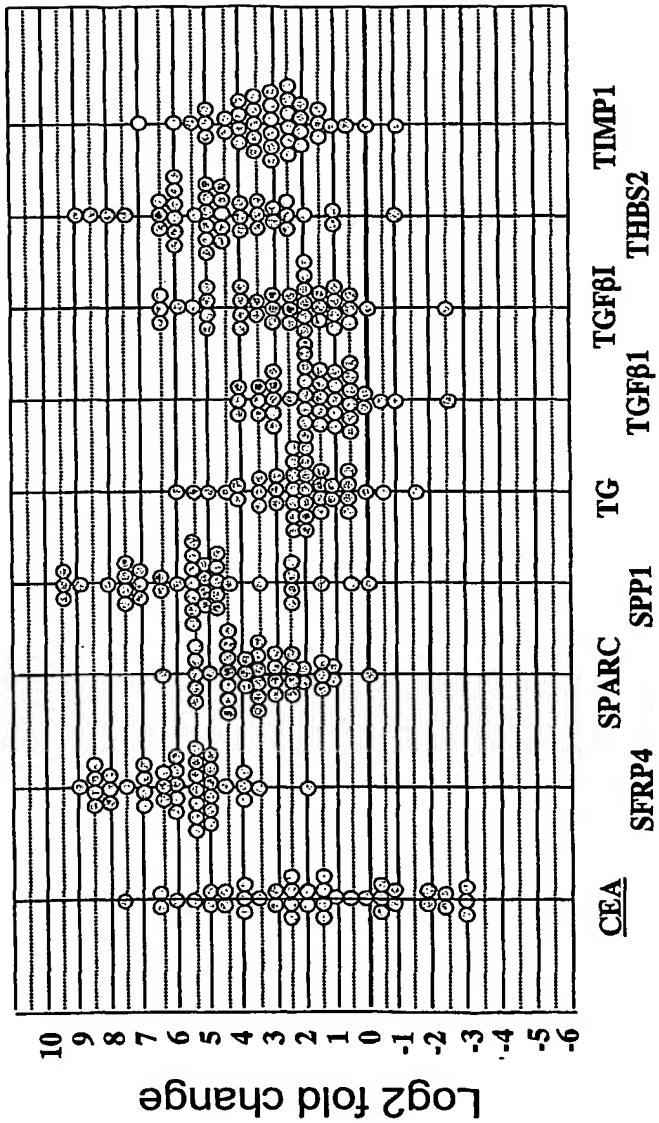

Log2 fold change
10
9
8
7
6
5
4
3
2
1
0
-1
-2
-3
-4
-5
-6
CEA
SFRP4
SPARC
SPP1
TG
TGFβ1
TGFβI
THBS2
TIMP1

Fig. 9c

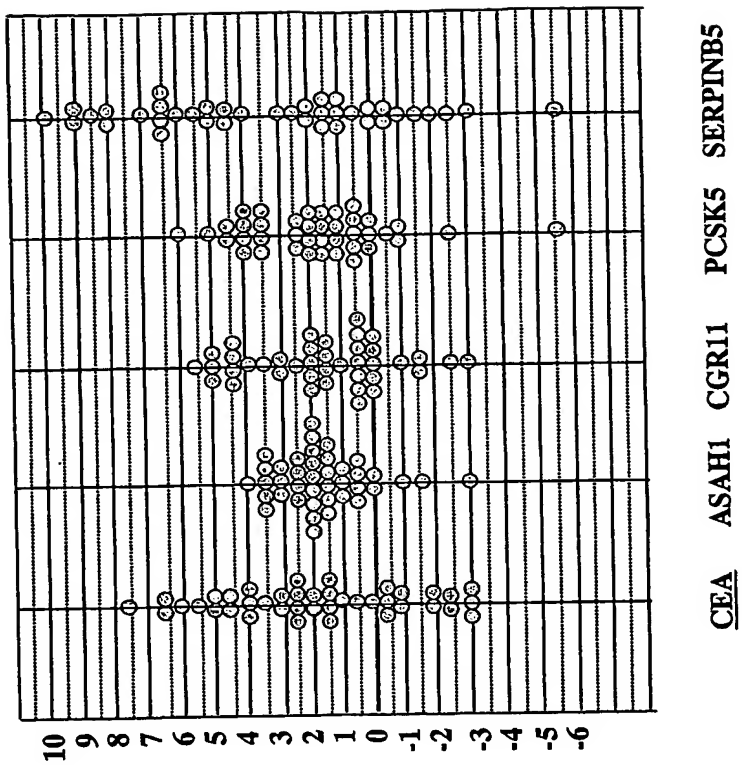

Log2 fold change
10
9
8
7
6
5
4
3
2
1
0
-1
-2
-3
-4
-5
-6
CEA
ASAH1
CGR11
PCSK5
SERPINB5

Fig. 9d

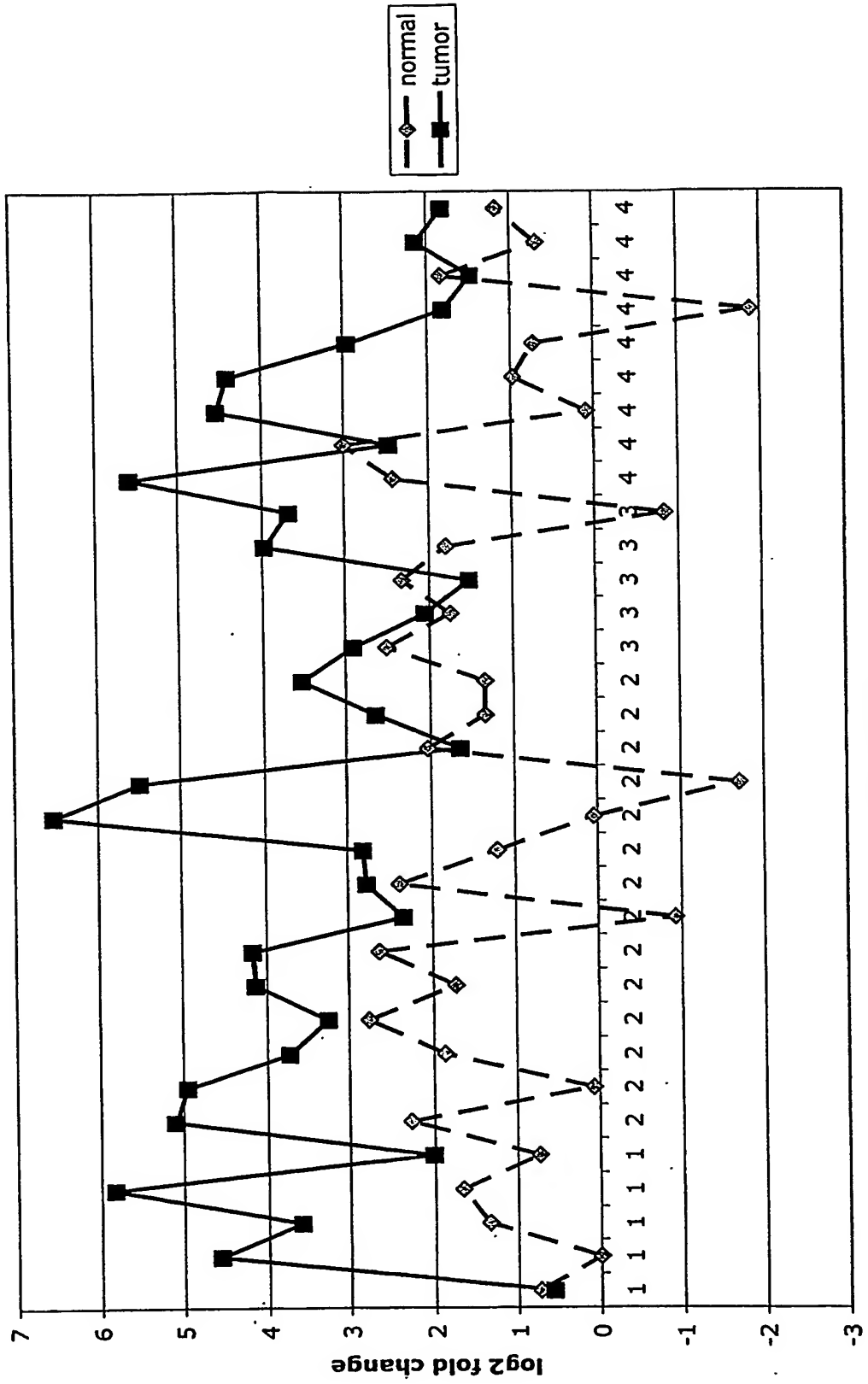


Fig. 10a adlican

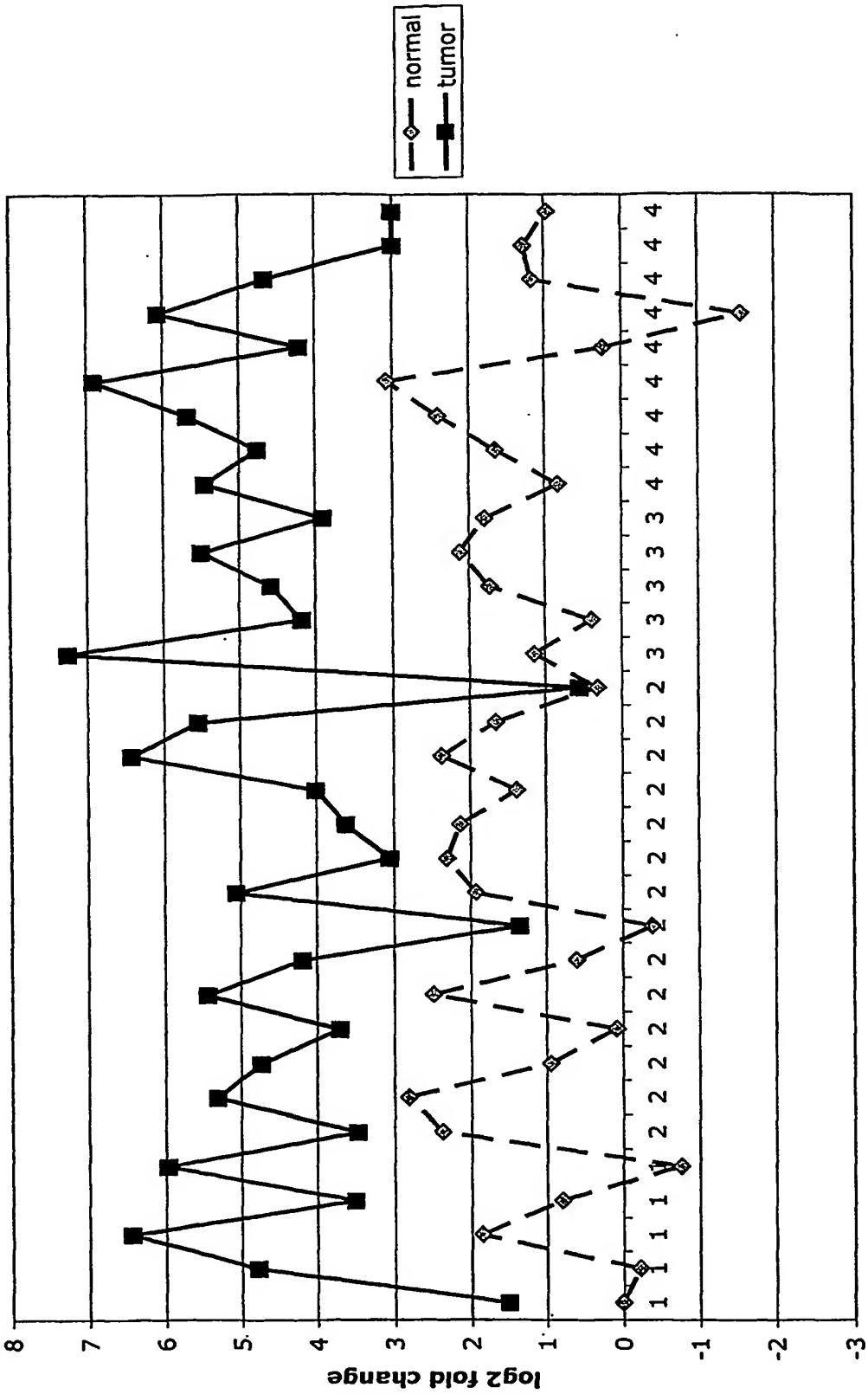


Fig. 10b ASPN

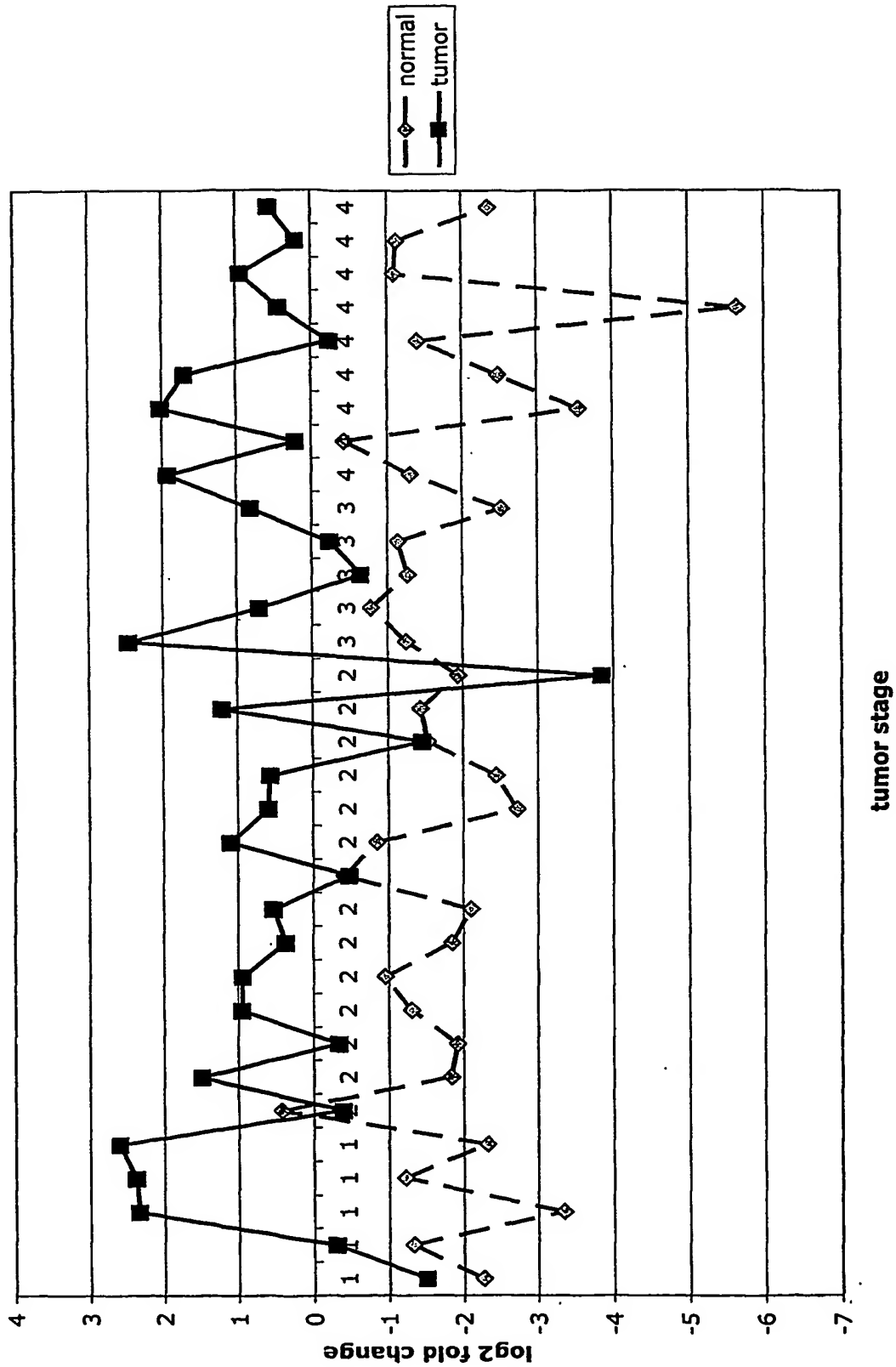


Fig. 10c CSPG2

Fig. 10d CST1,2,4

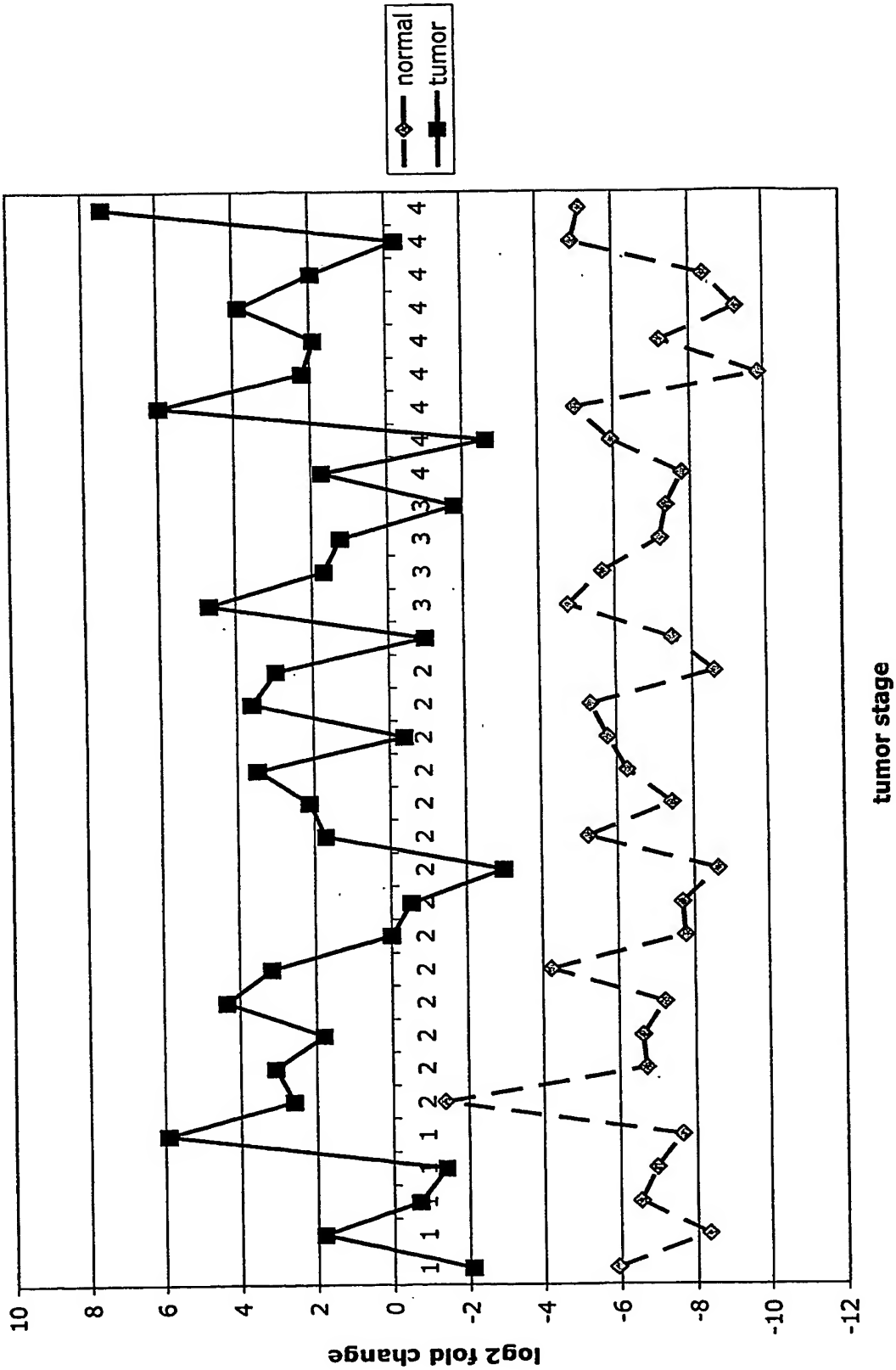


Fig. 10e EFEMP2

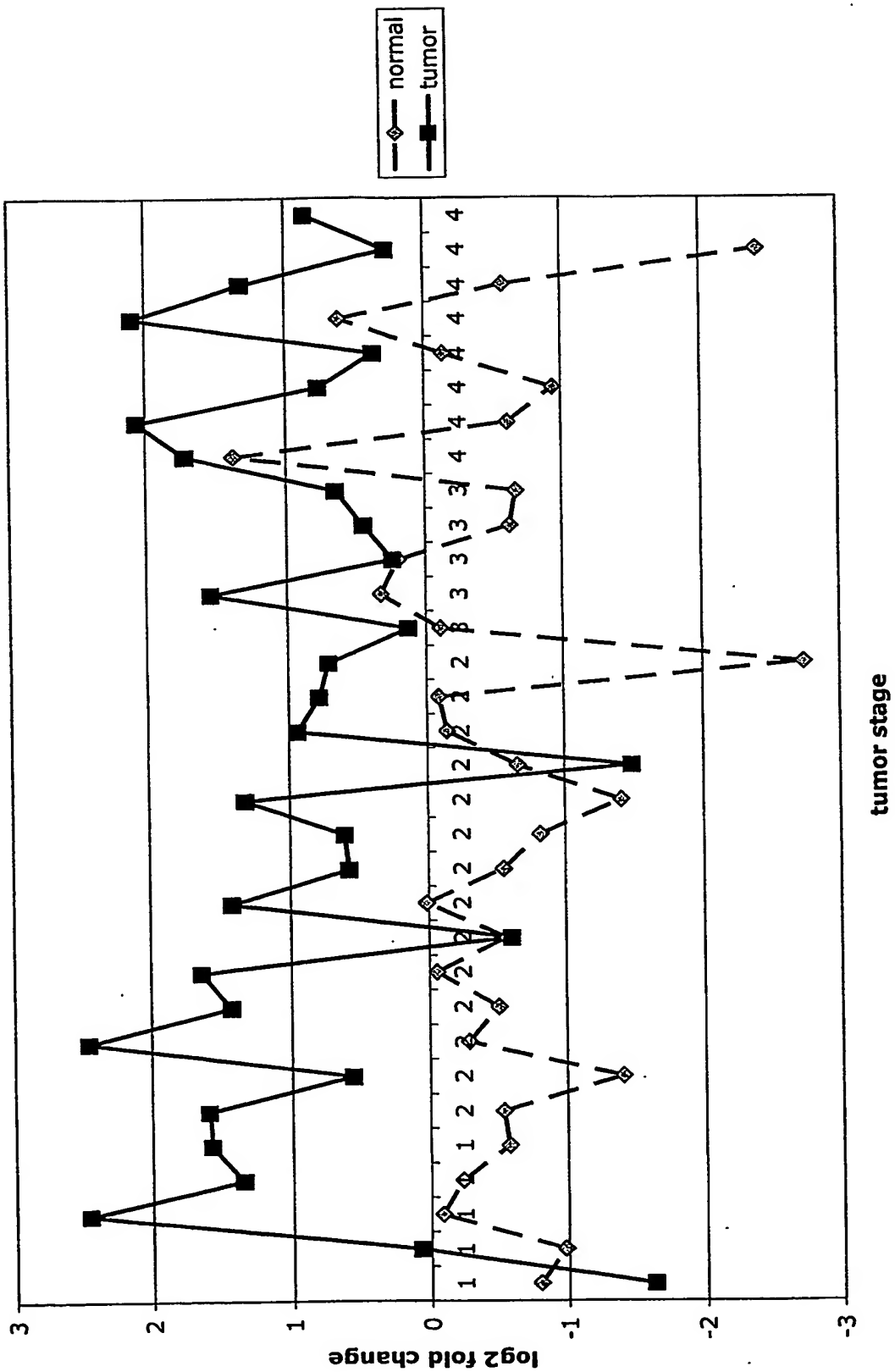
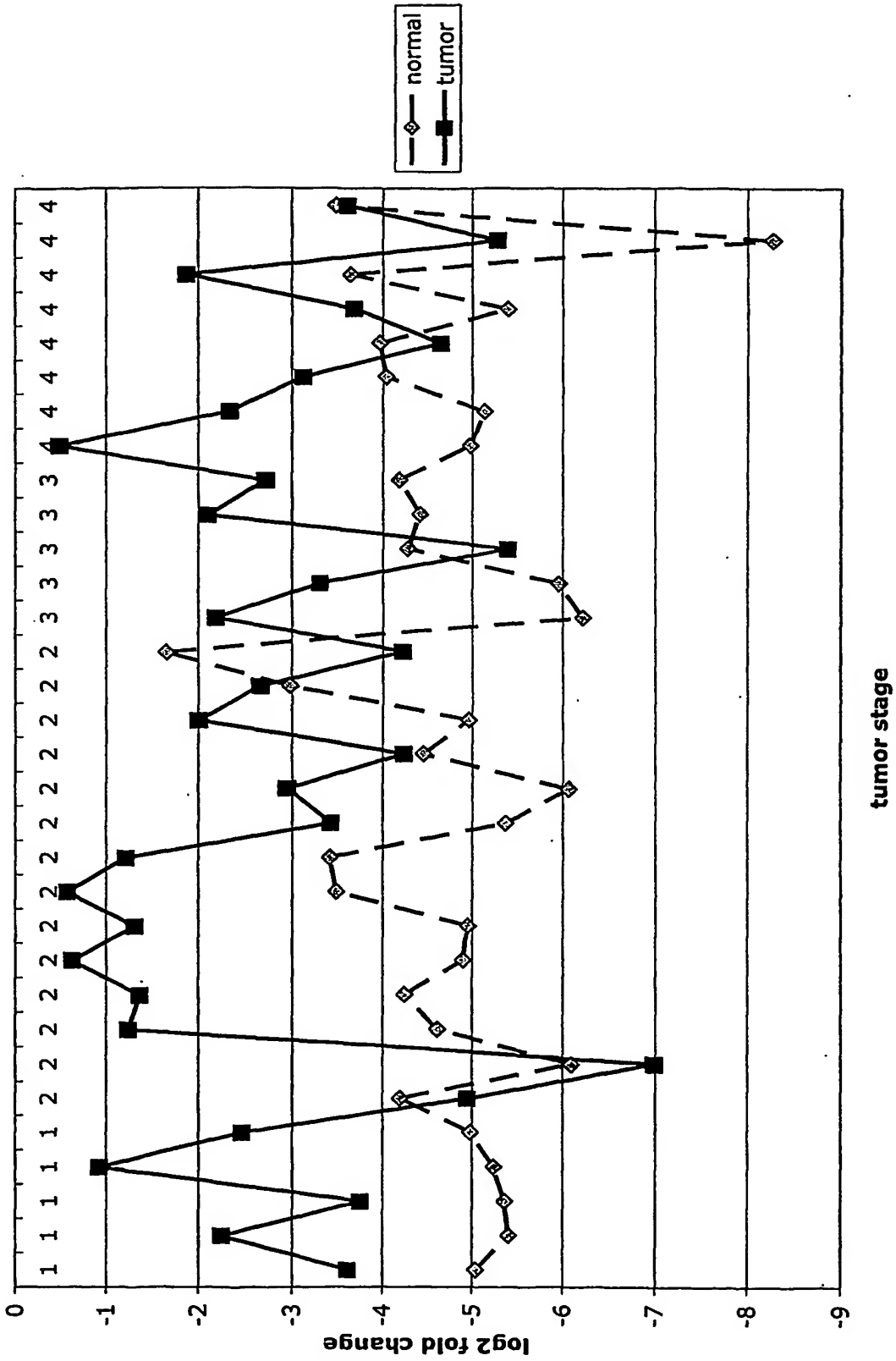


Fig. 10f GGH


normal
tumor
log2 fold change
0
-1
-2
-3
-4
-5
-6
-7
-8
-9
1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 4 4 4 4 4 4 4 4 4 4 4
tumor stage

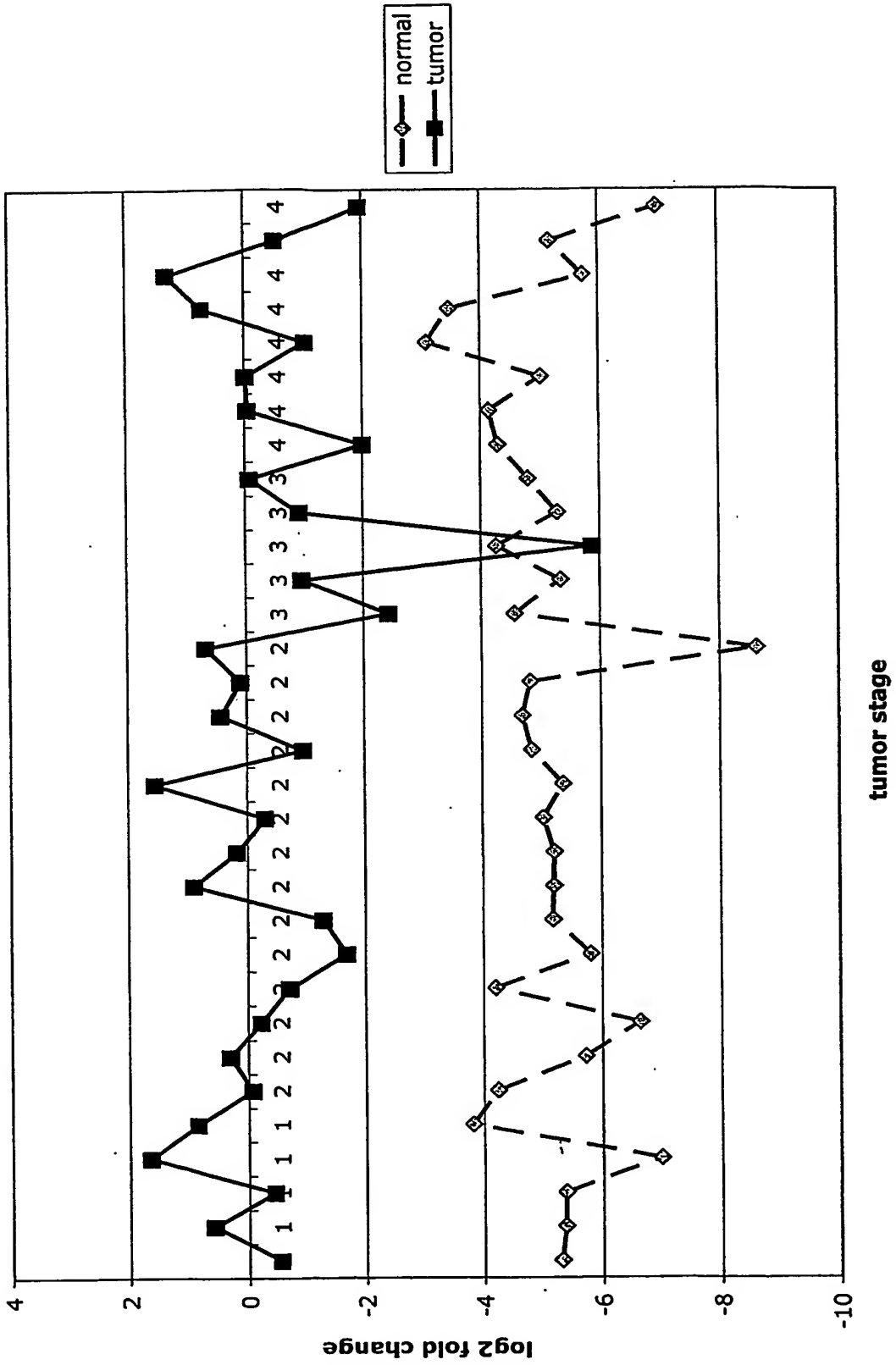
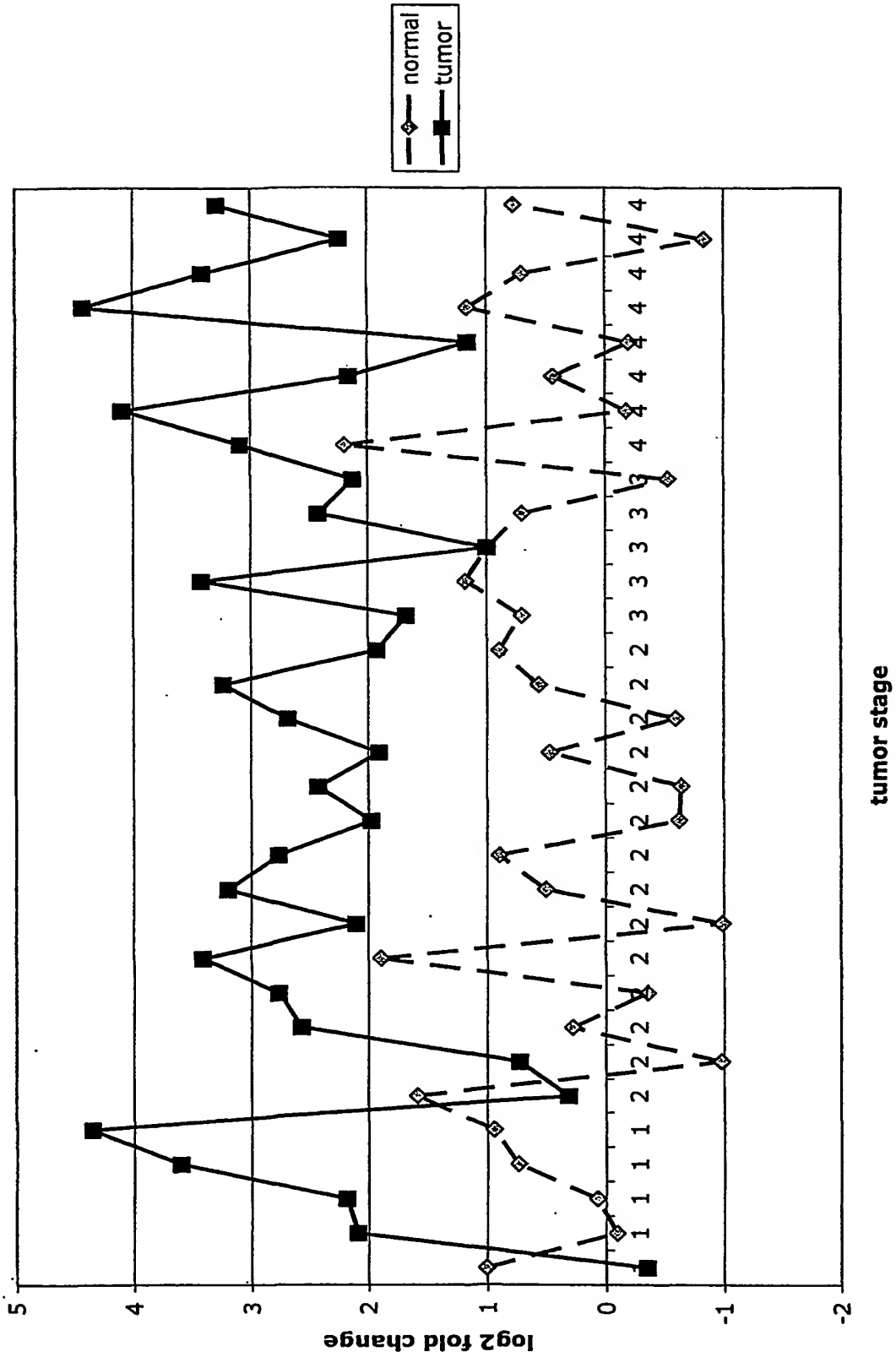


Fig. 10g INHBA

Fig. 10h IGFBP7



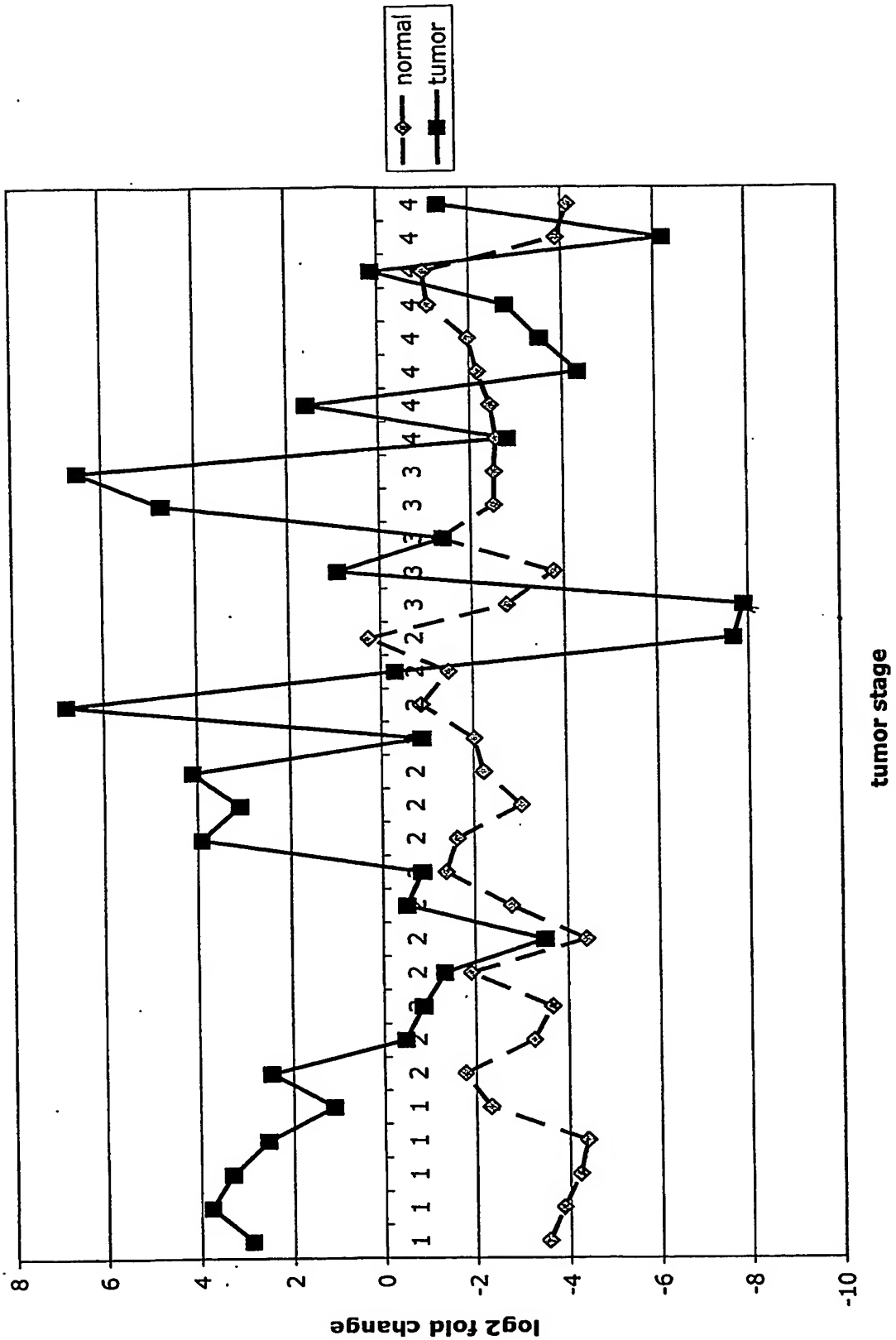


Fig. 10i KLK10

Fig. 10j LEPRE1

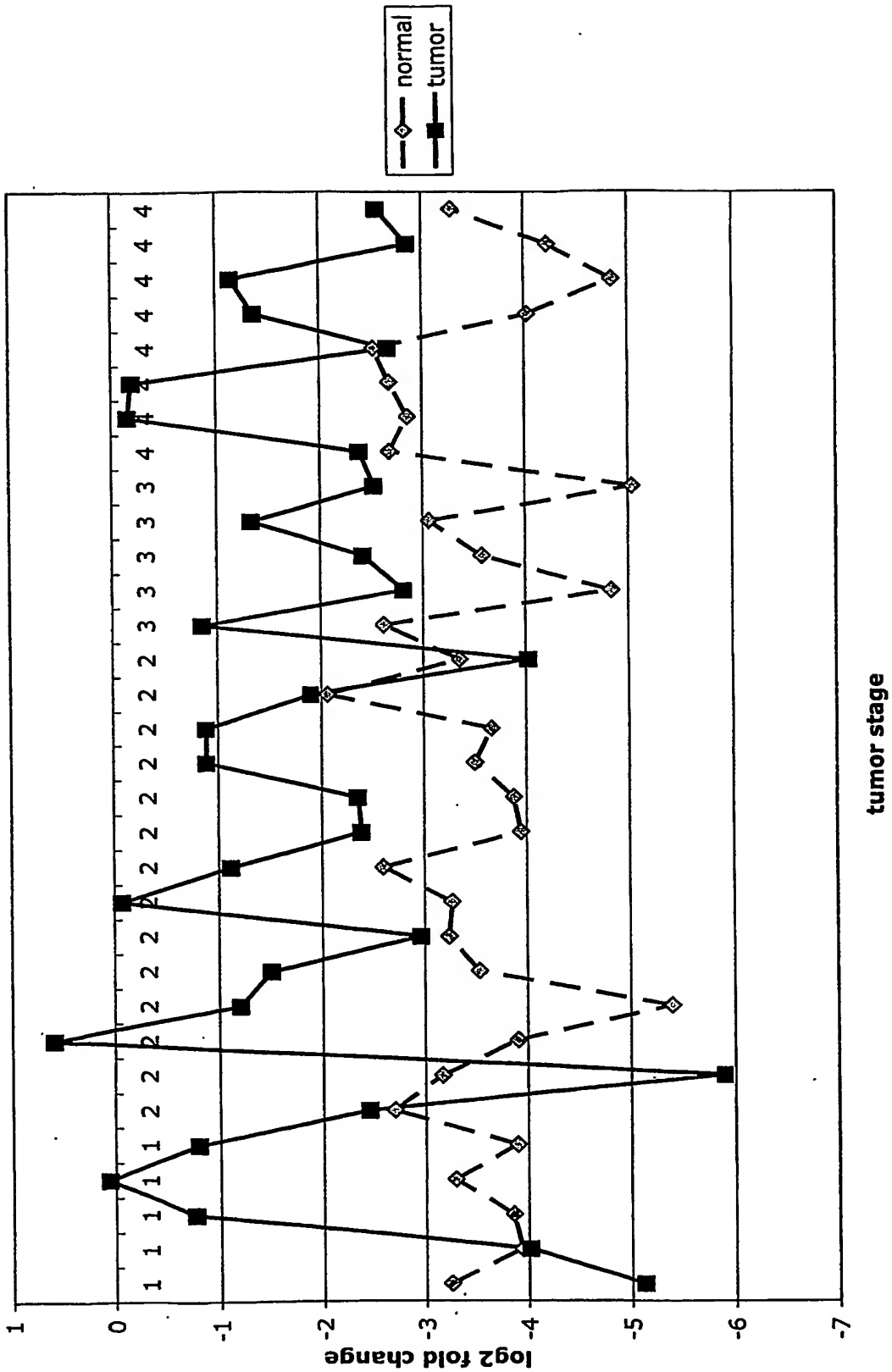
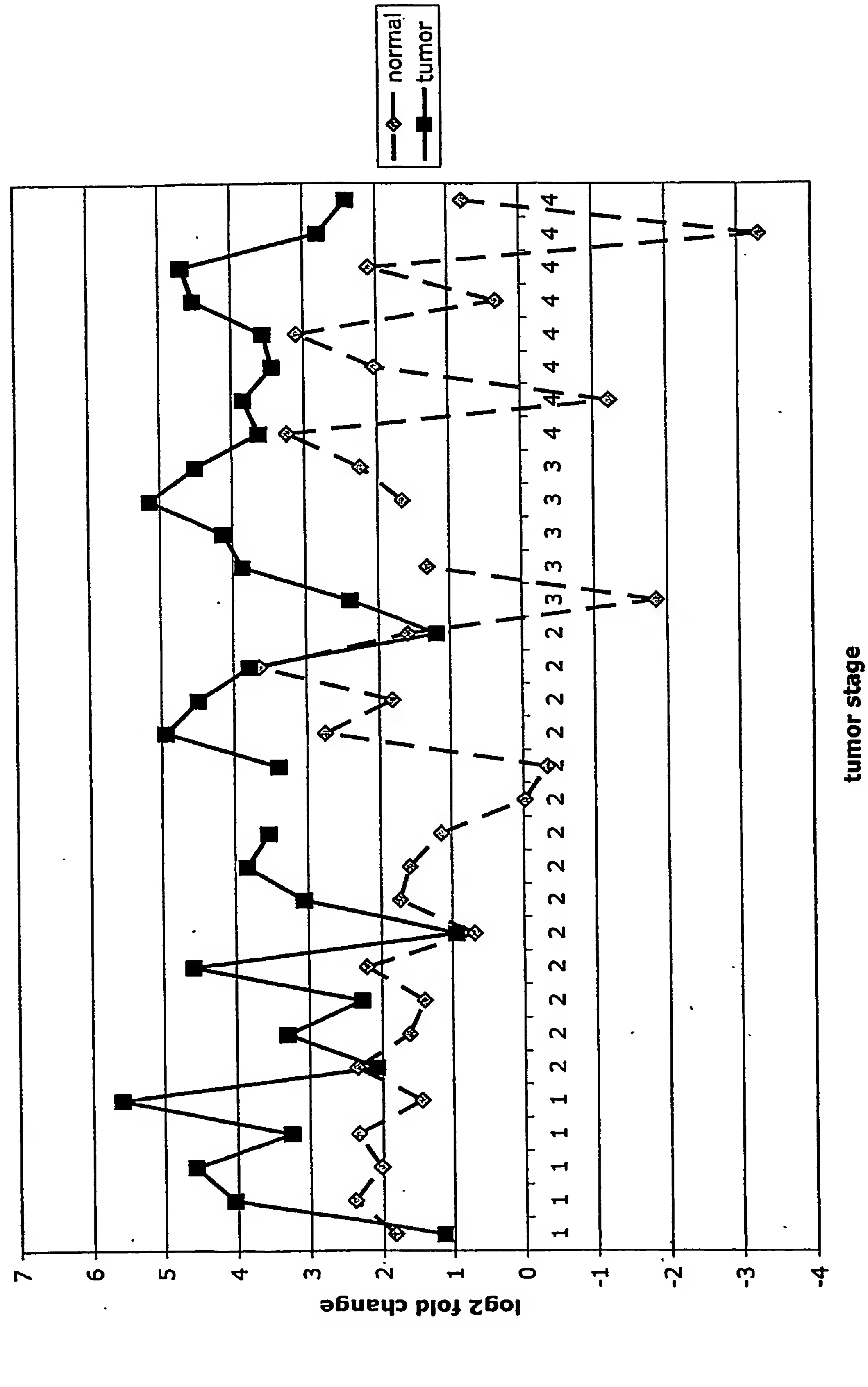


Fig. 10k LUM


normal
tumor
log2 fold change
7
6
5
4
3
2
1
0
-1
-2
-3
-4
tumor stage
1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 3 3 3 3 3 4 4 4 4 4 4 4 4

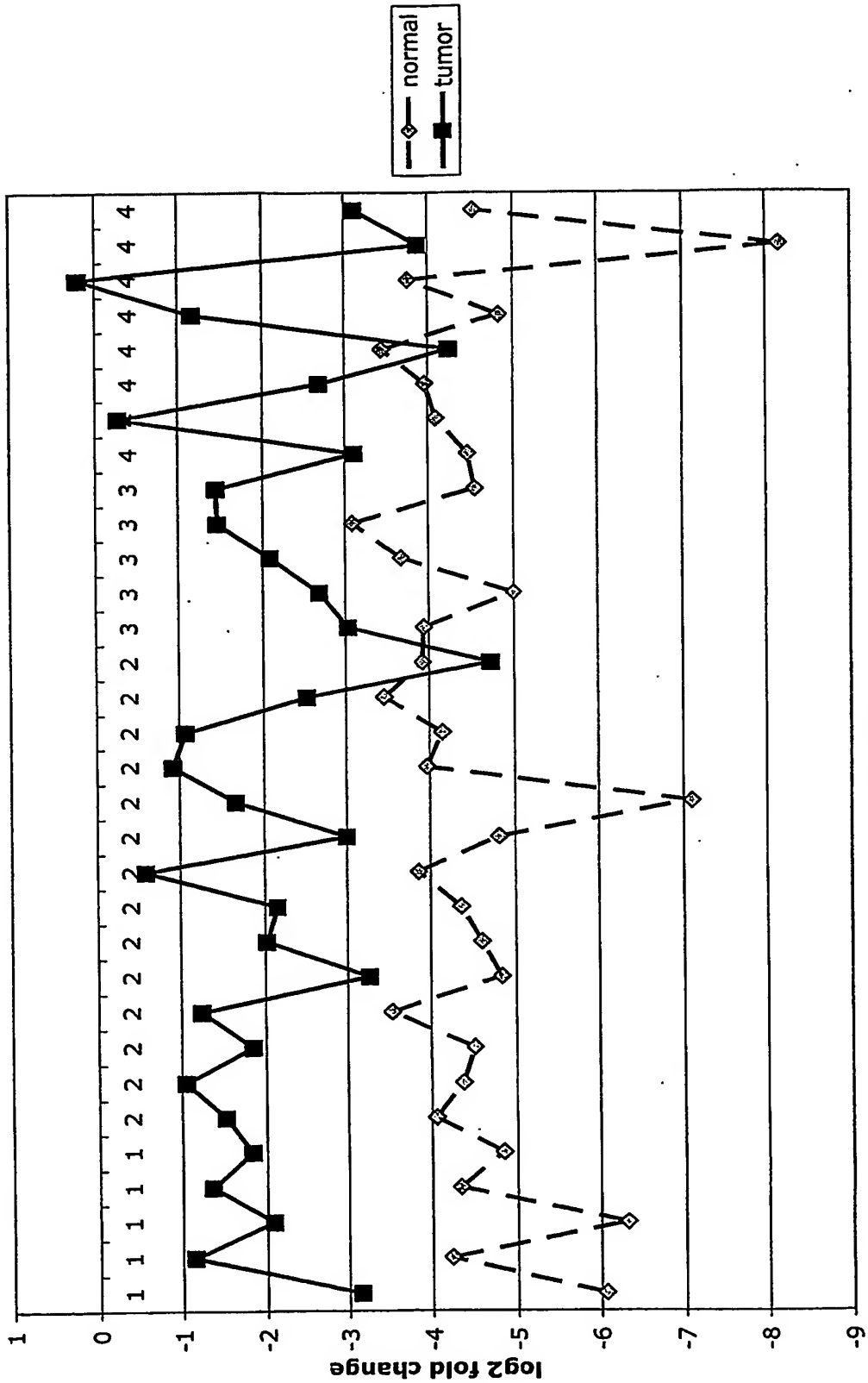


Fig. 10I LOXL2

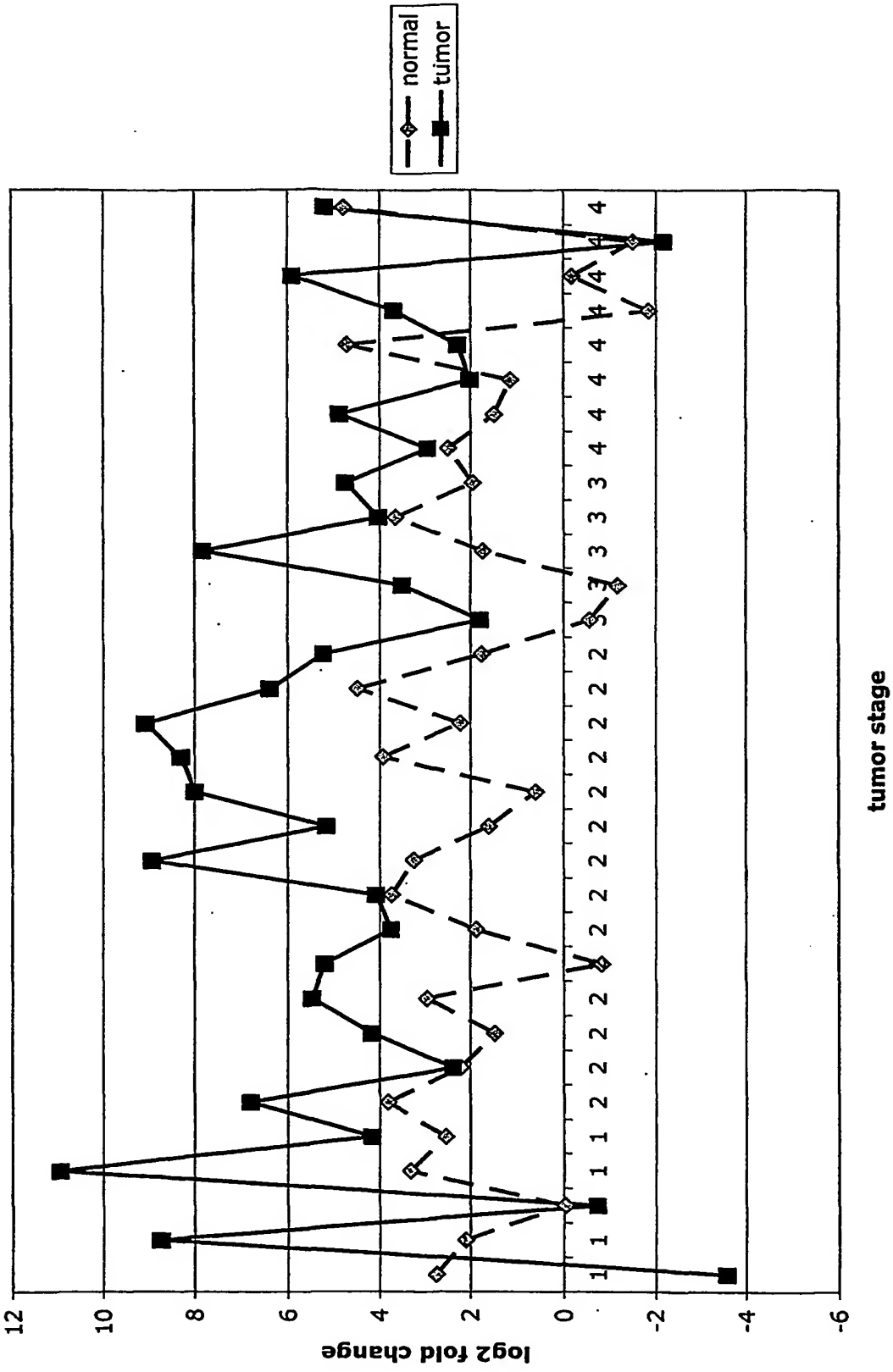


Fig. 10m MMP12

Fig.10n TIMP1

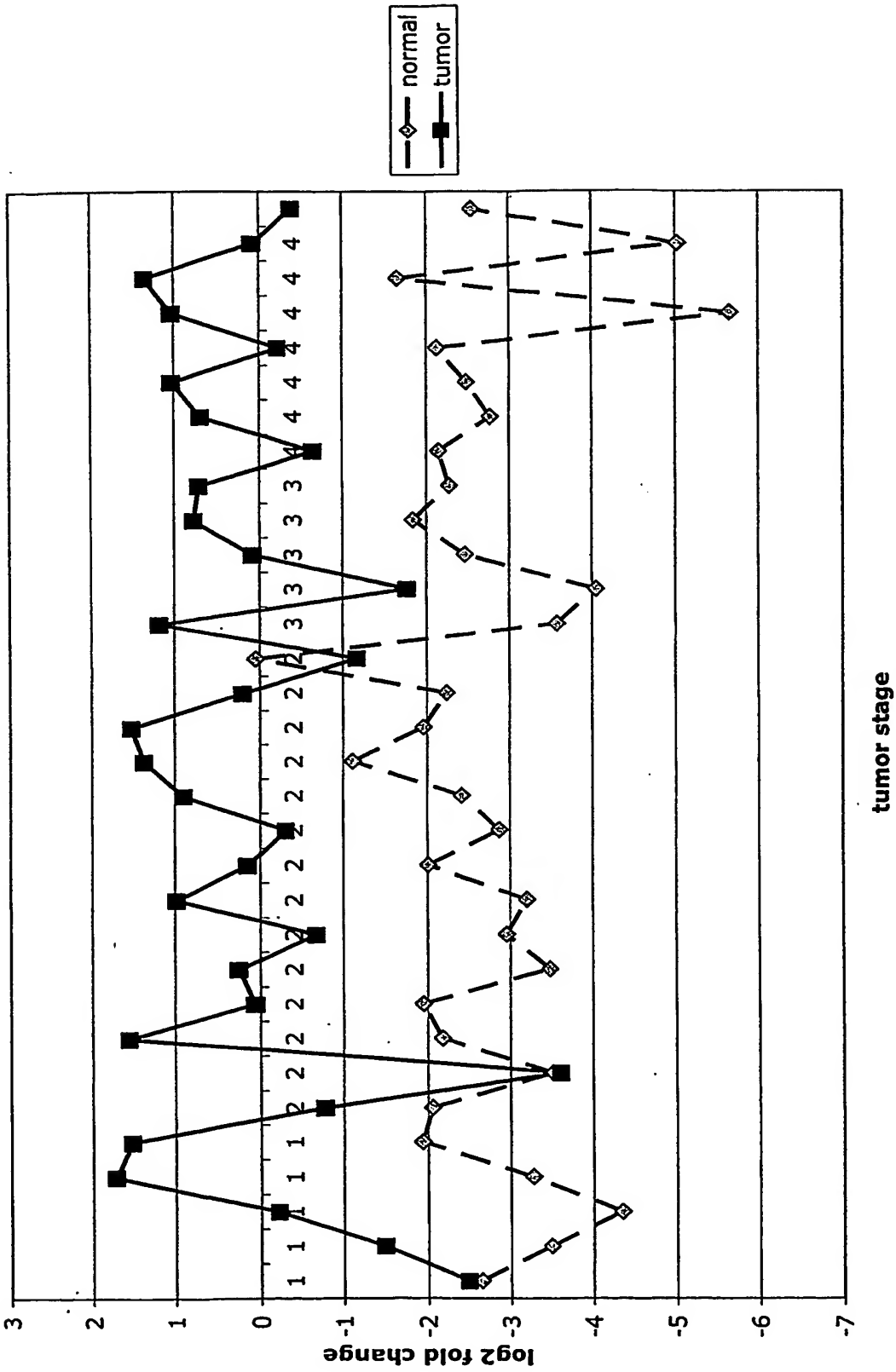


Fig. 10o ASAH1

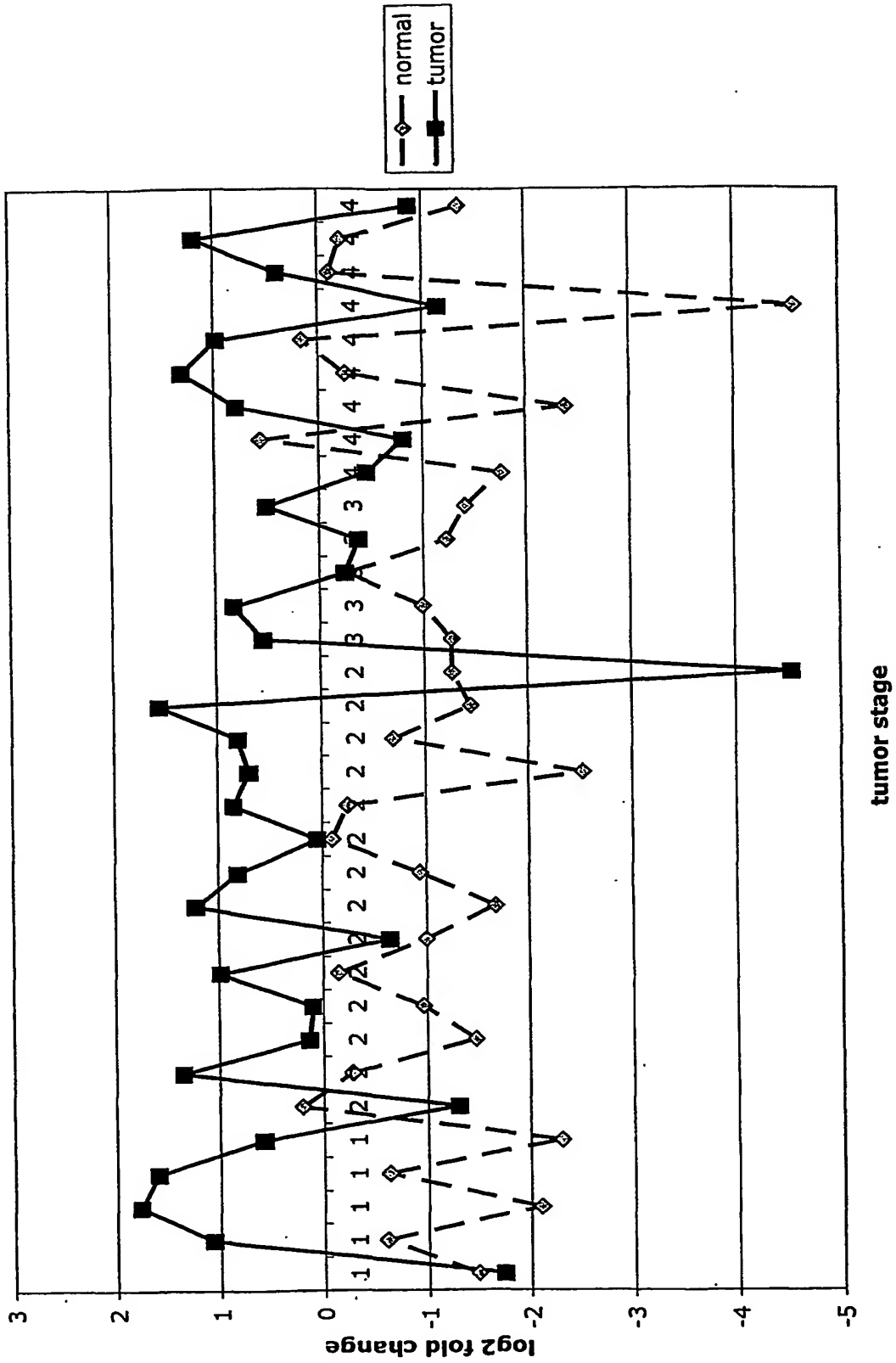


Fig. 10p SPP1

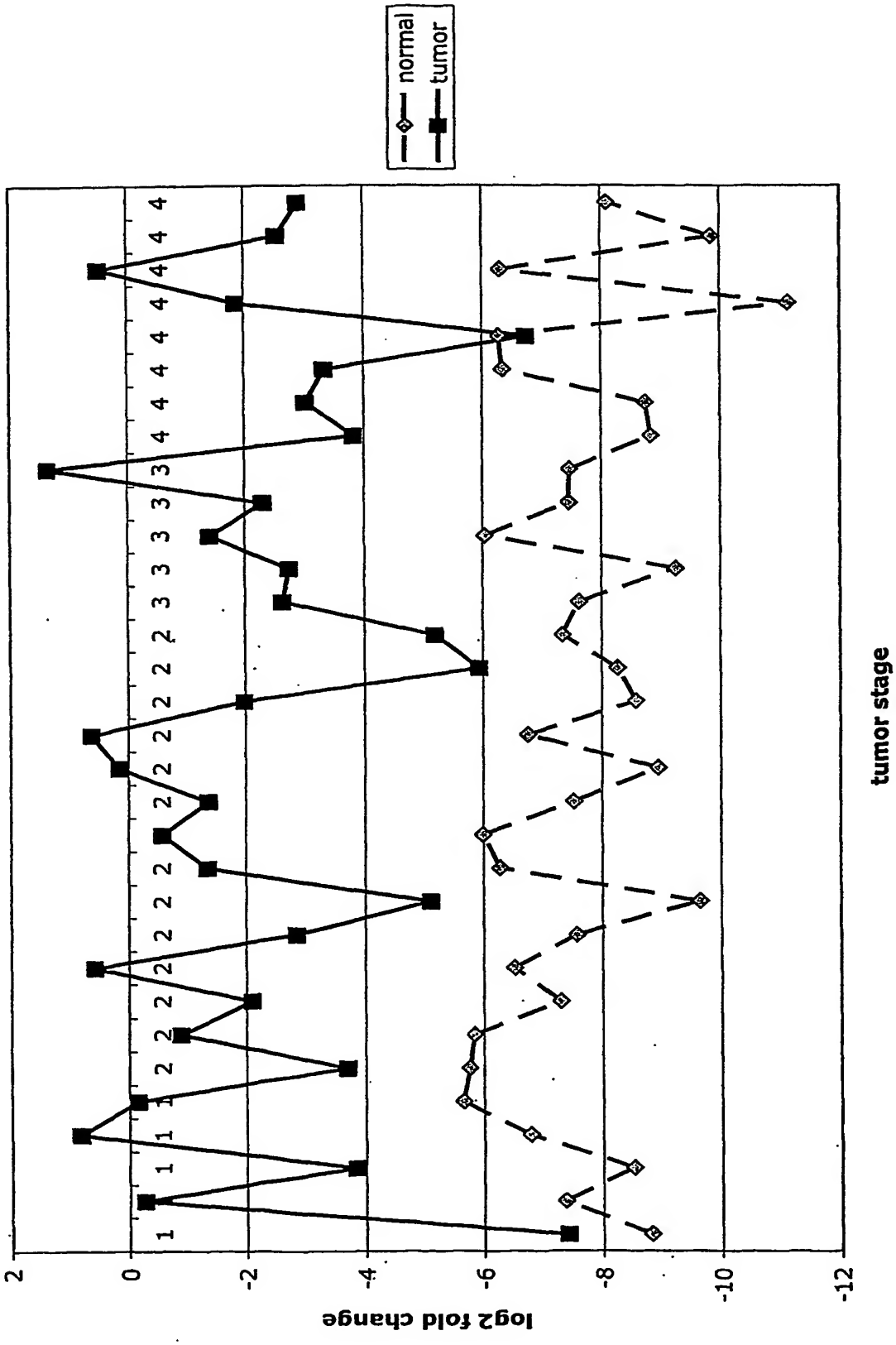
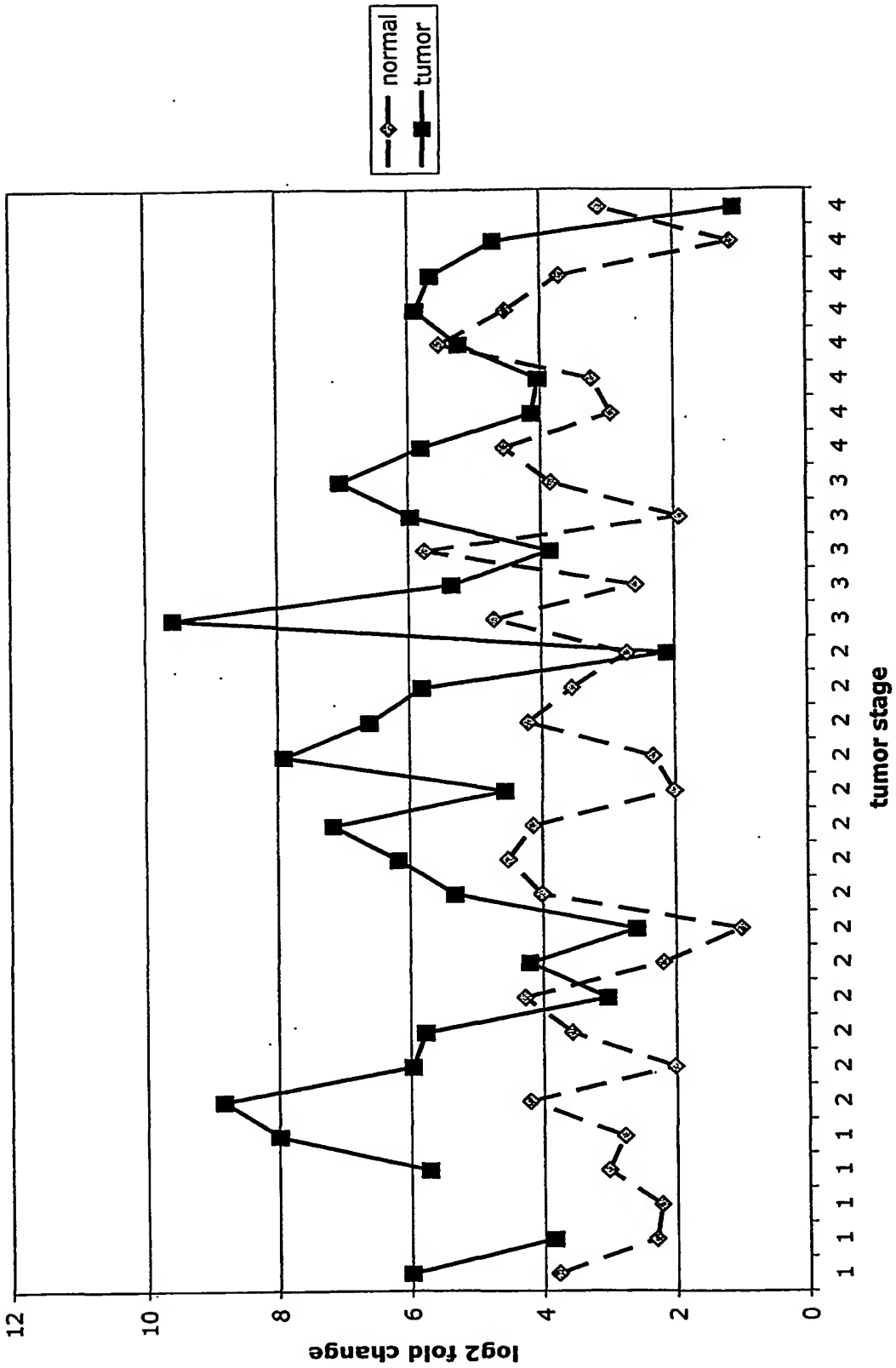


Fig. 10q SFRP2



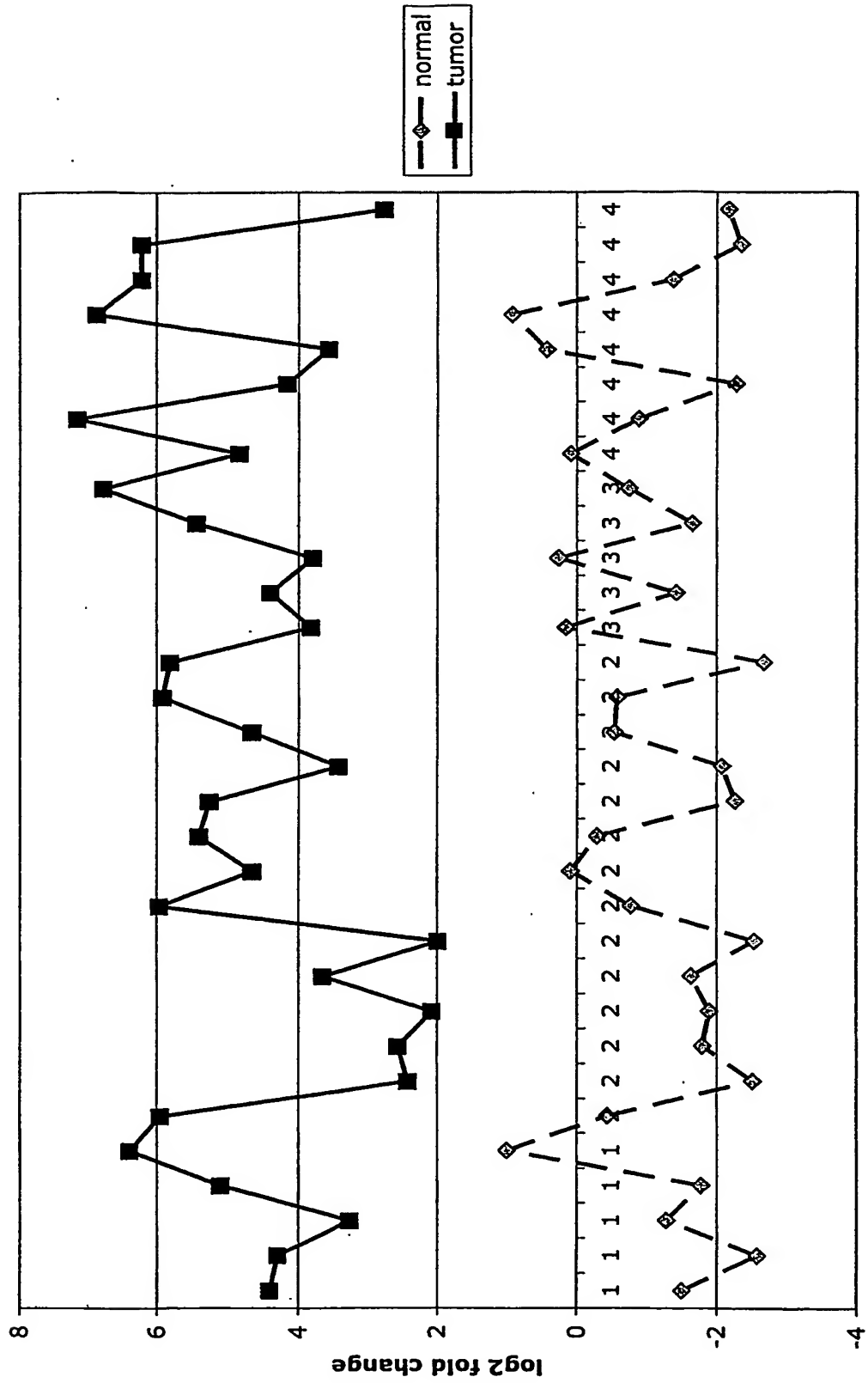
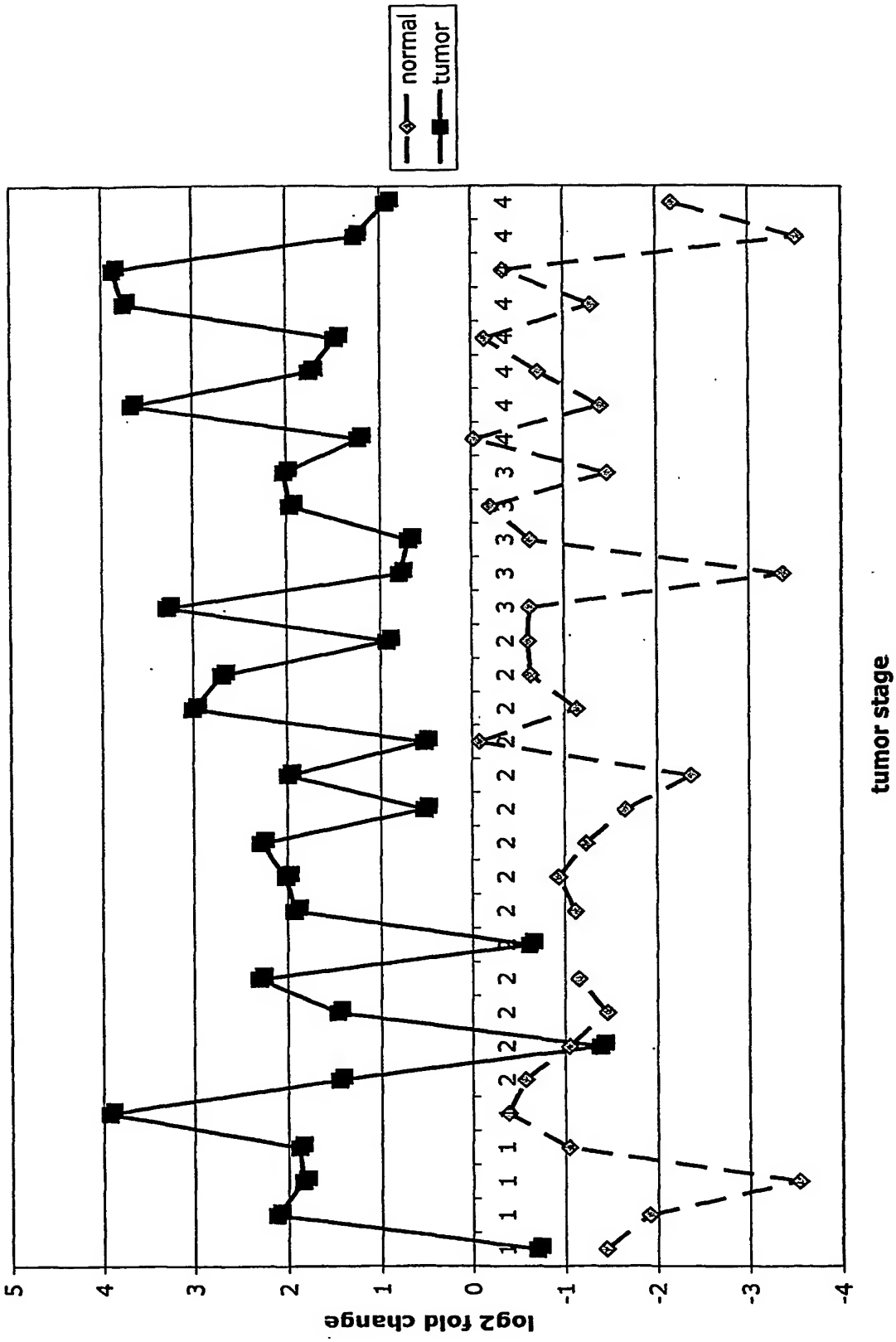


Fig. 10r SFRP4

Fig. 10s SPARC



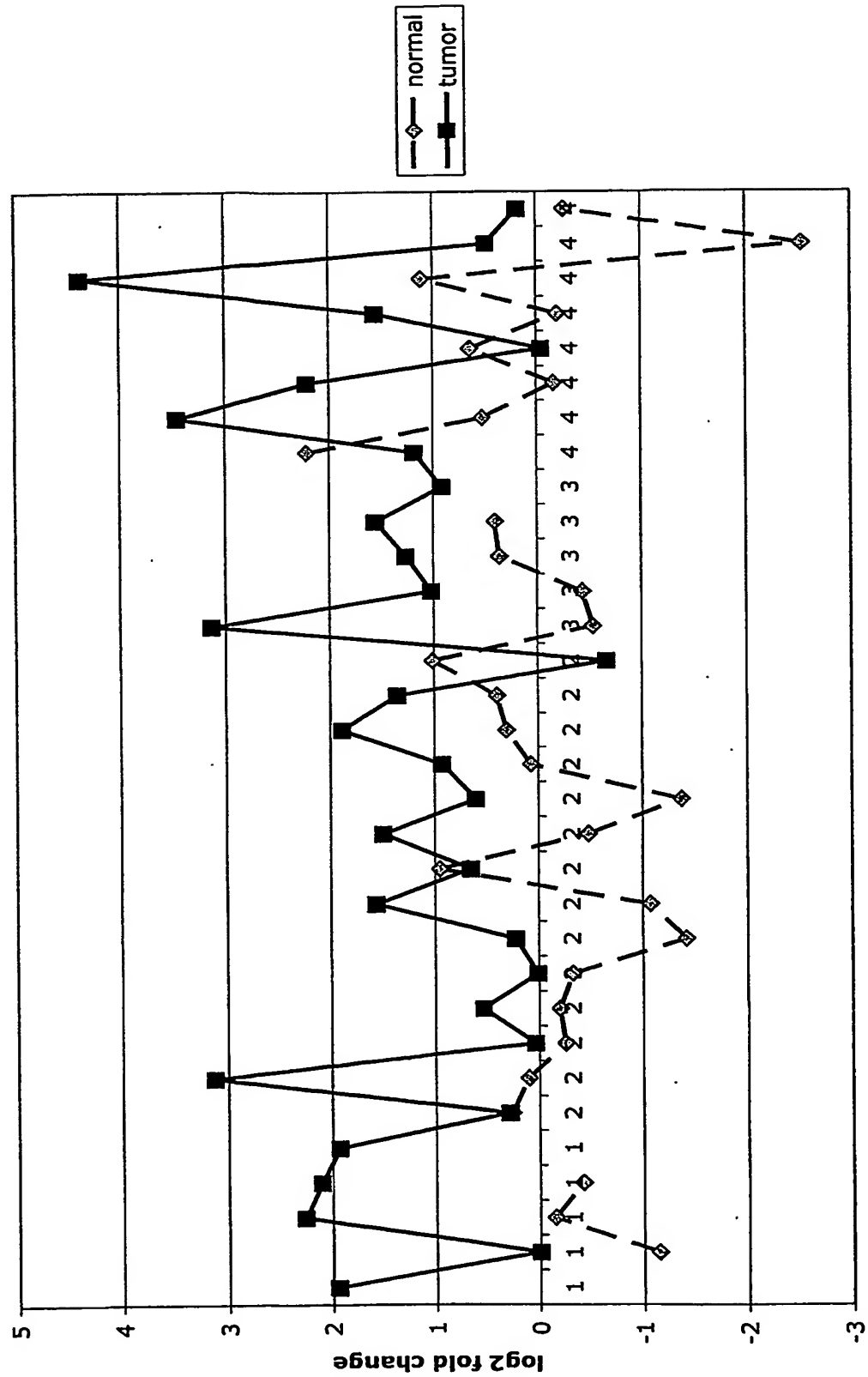


Fig. 10t PRSS11

Fig. 10u THBS2

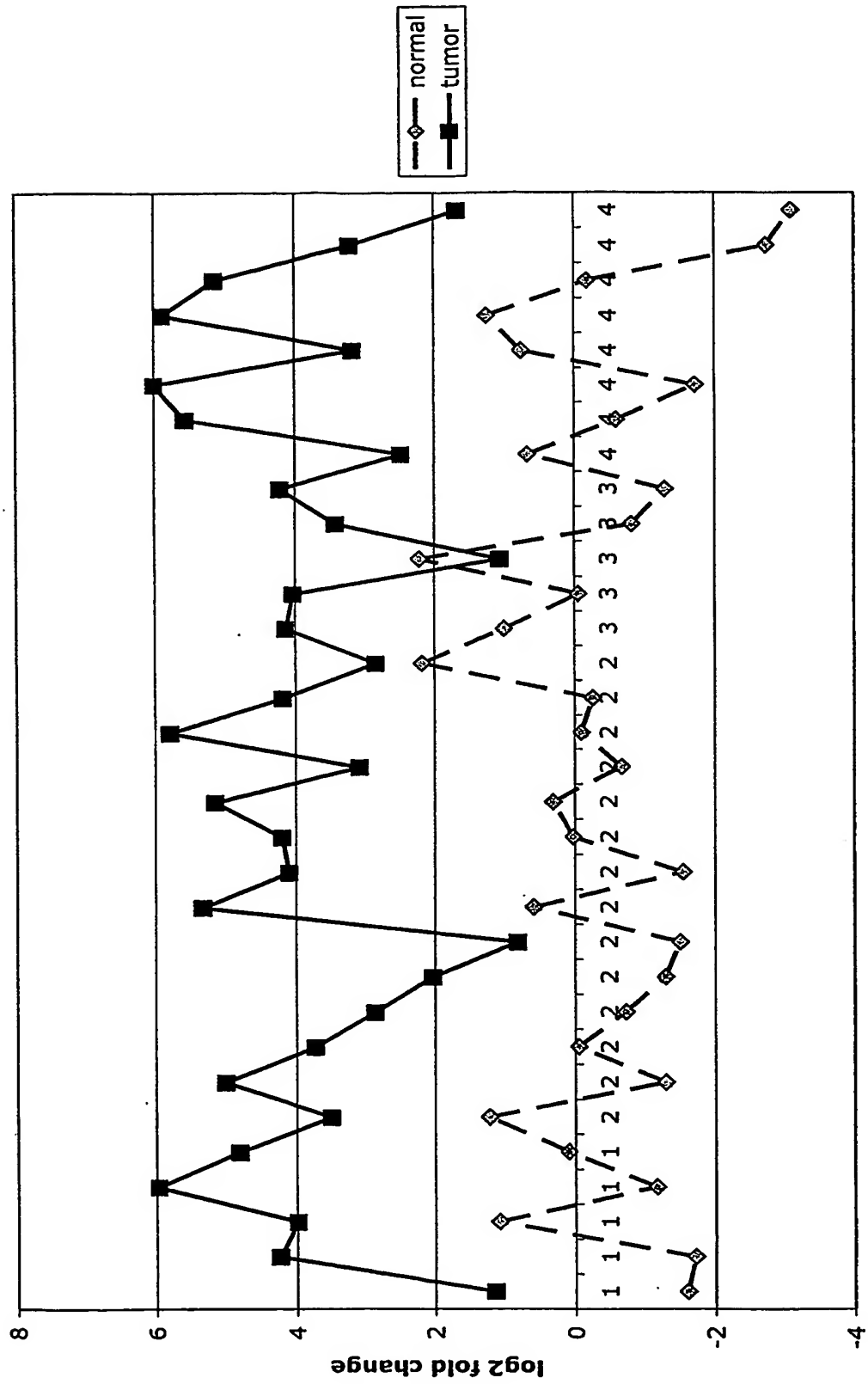
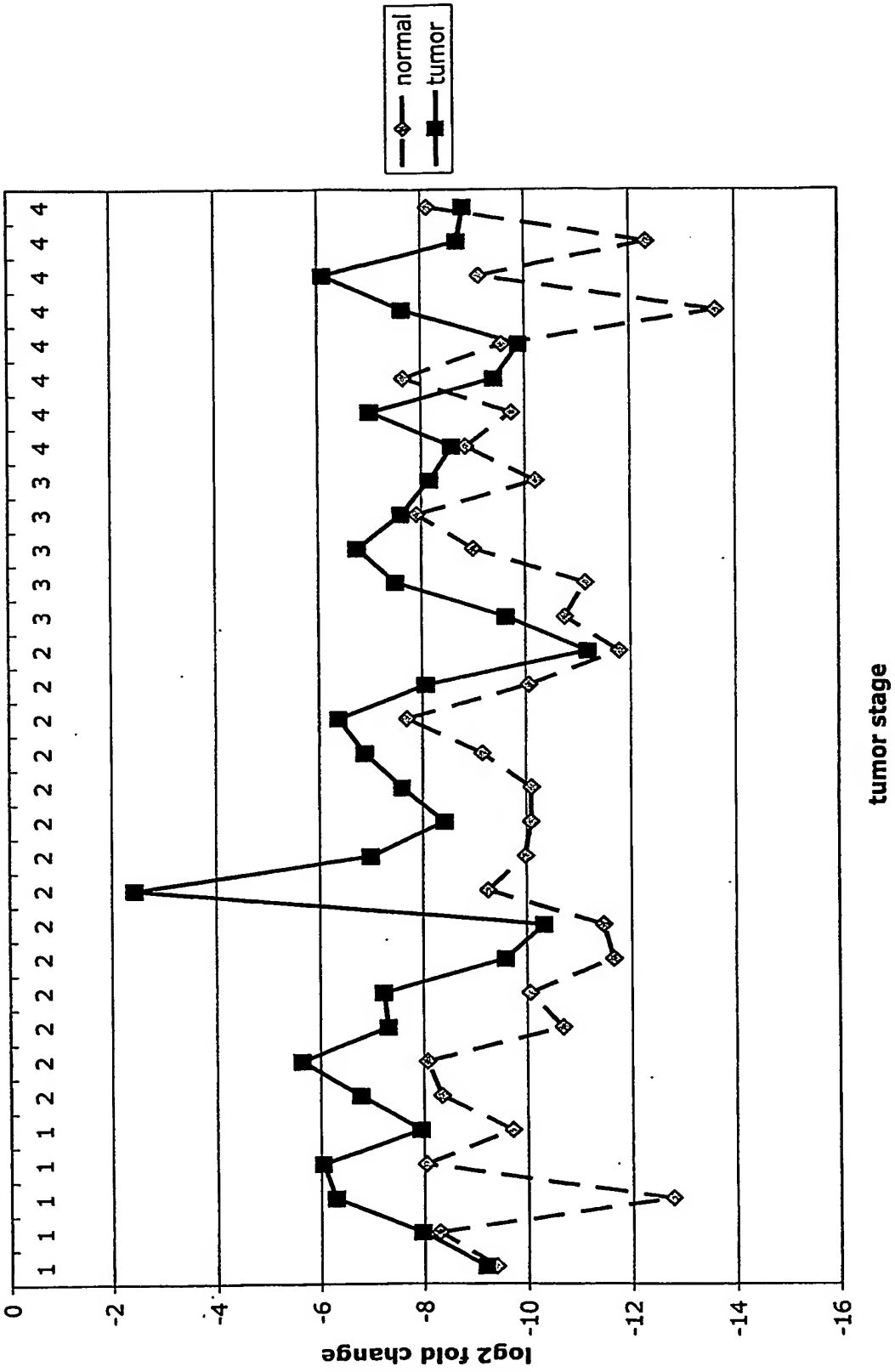


Fig. 10v TG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tumor stage

Fig. 10w TGFBI

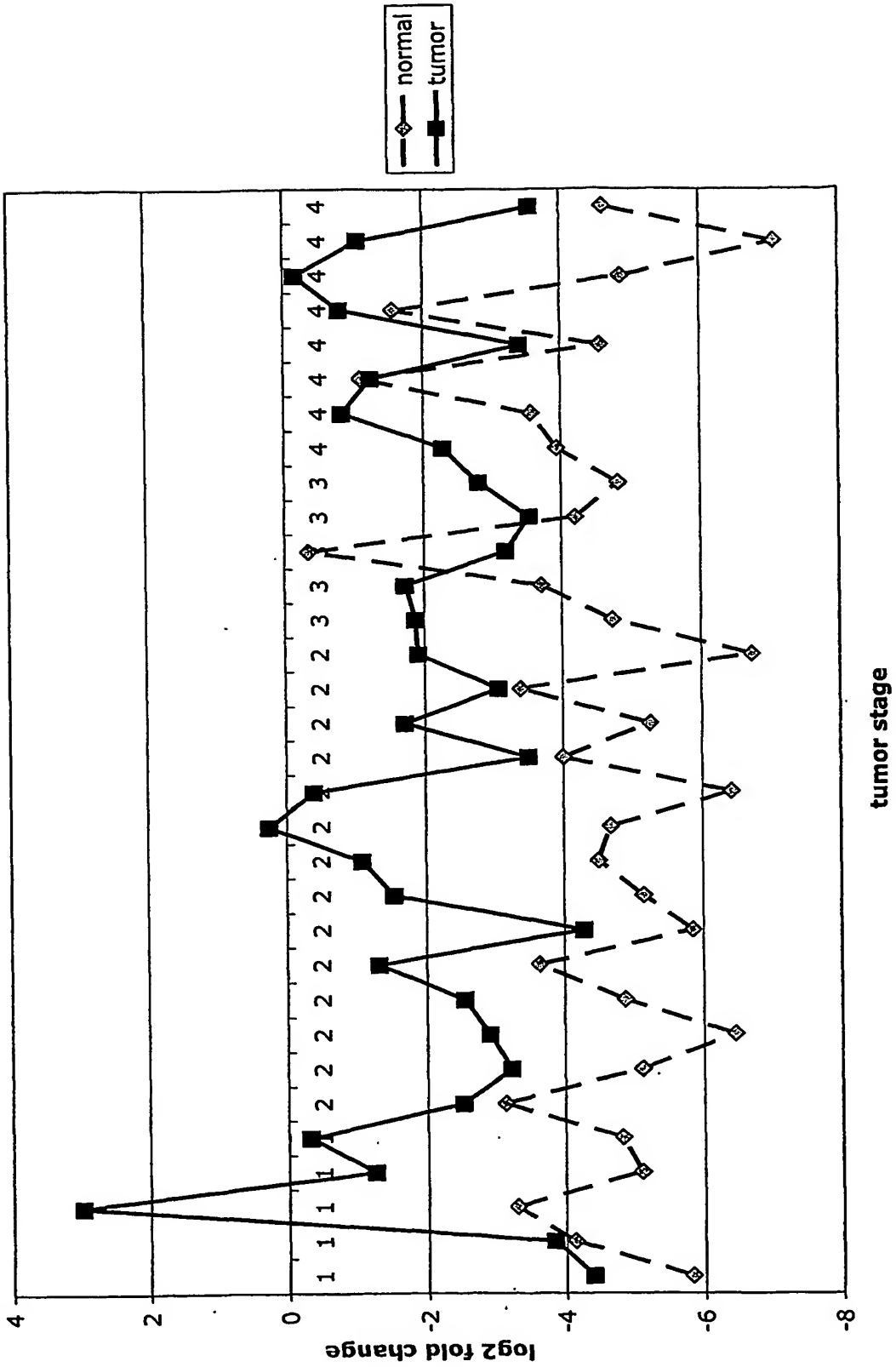


Fig. 10x CGR11

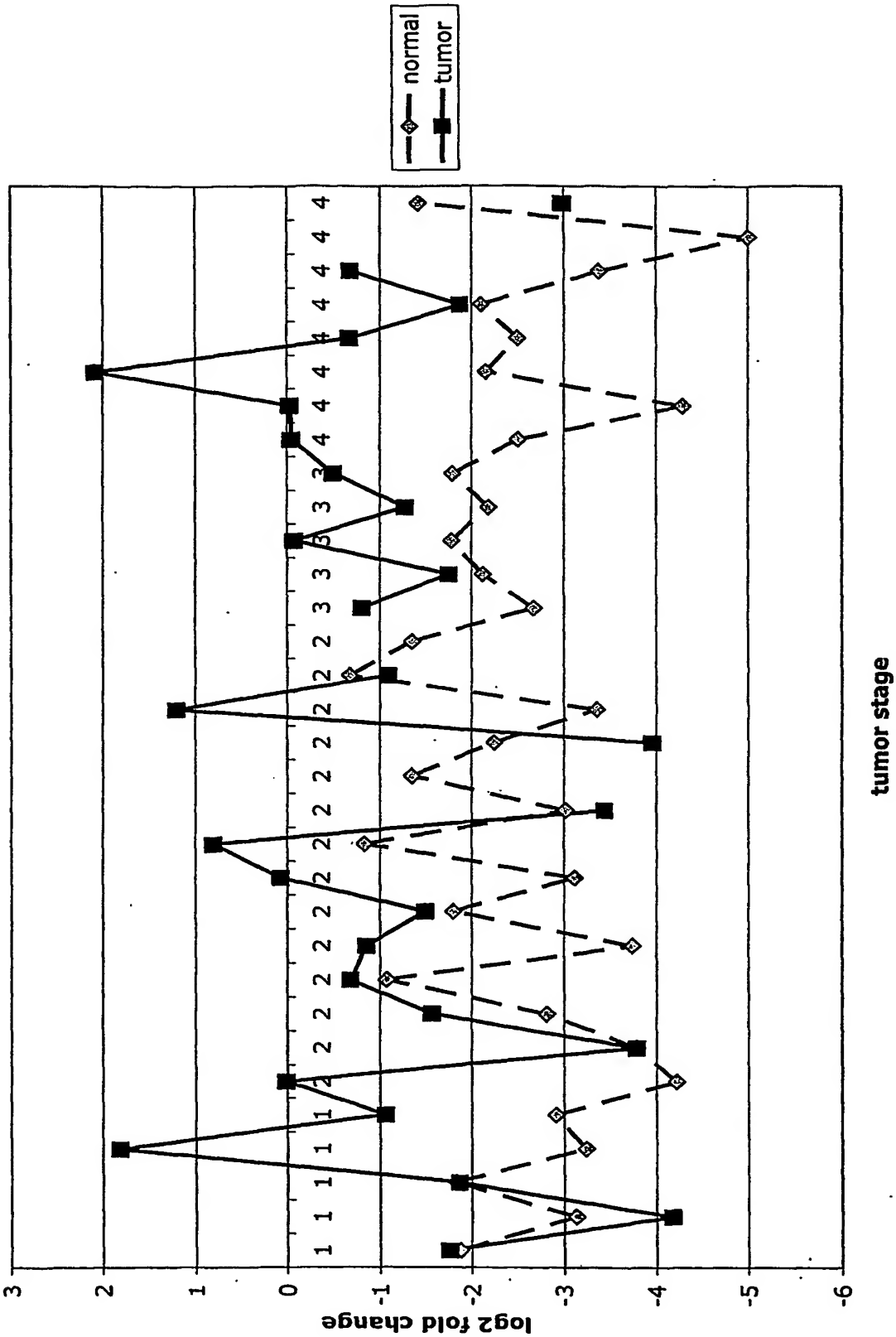


Fig. 10y SERPINH1

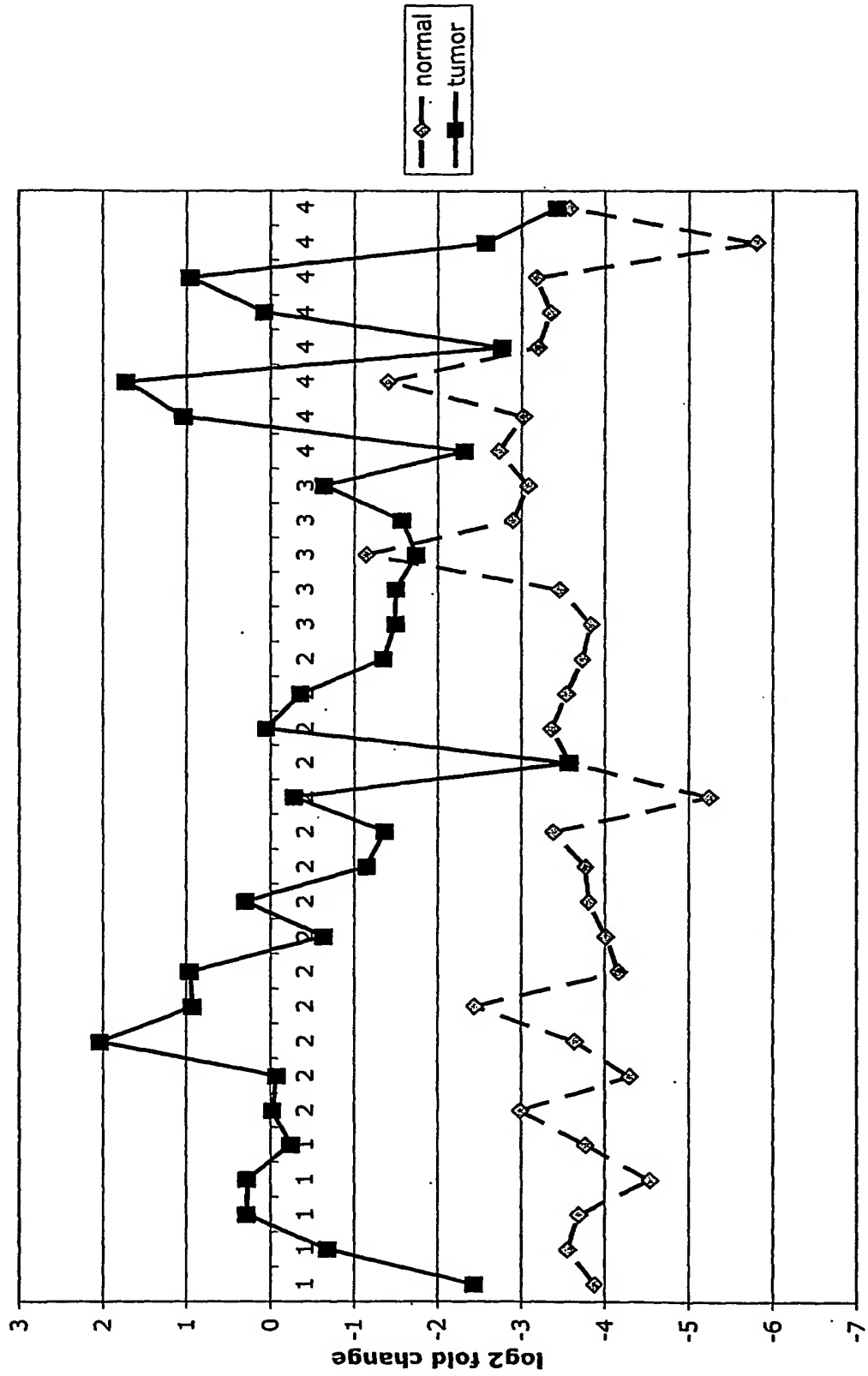
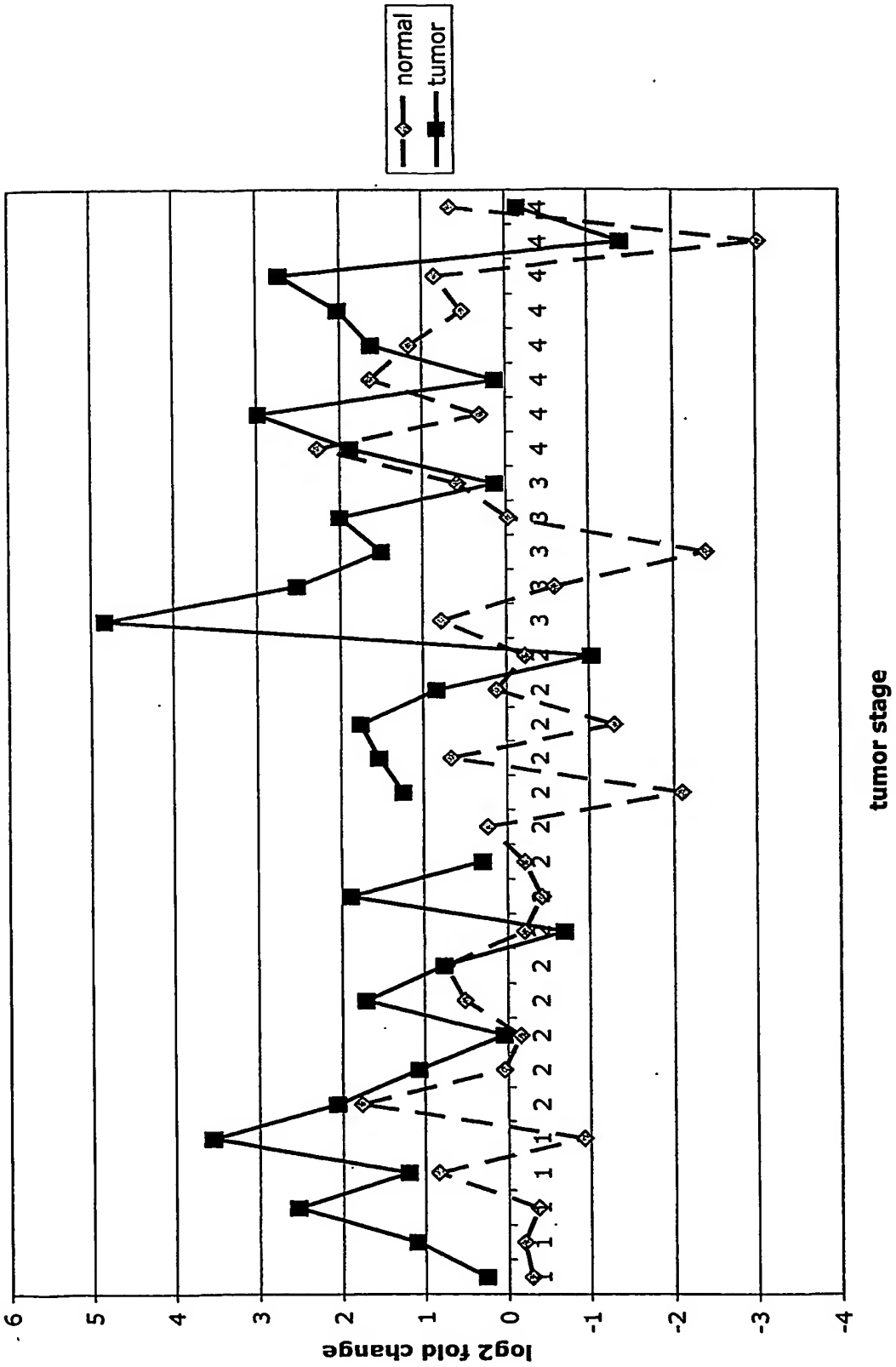


Fig. 10z MMP2



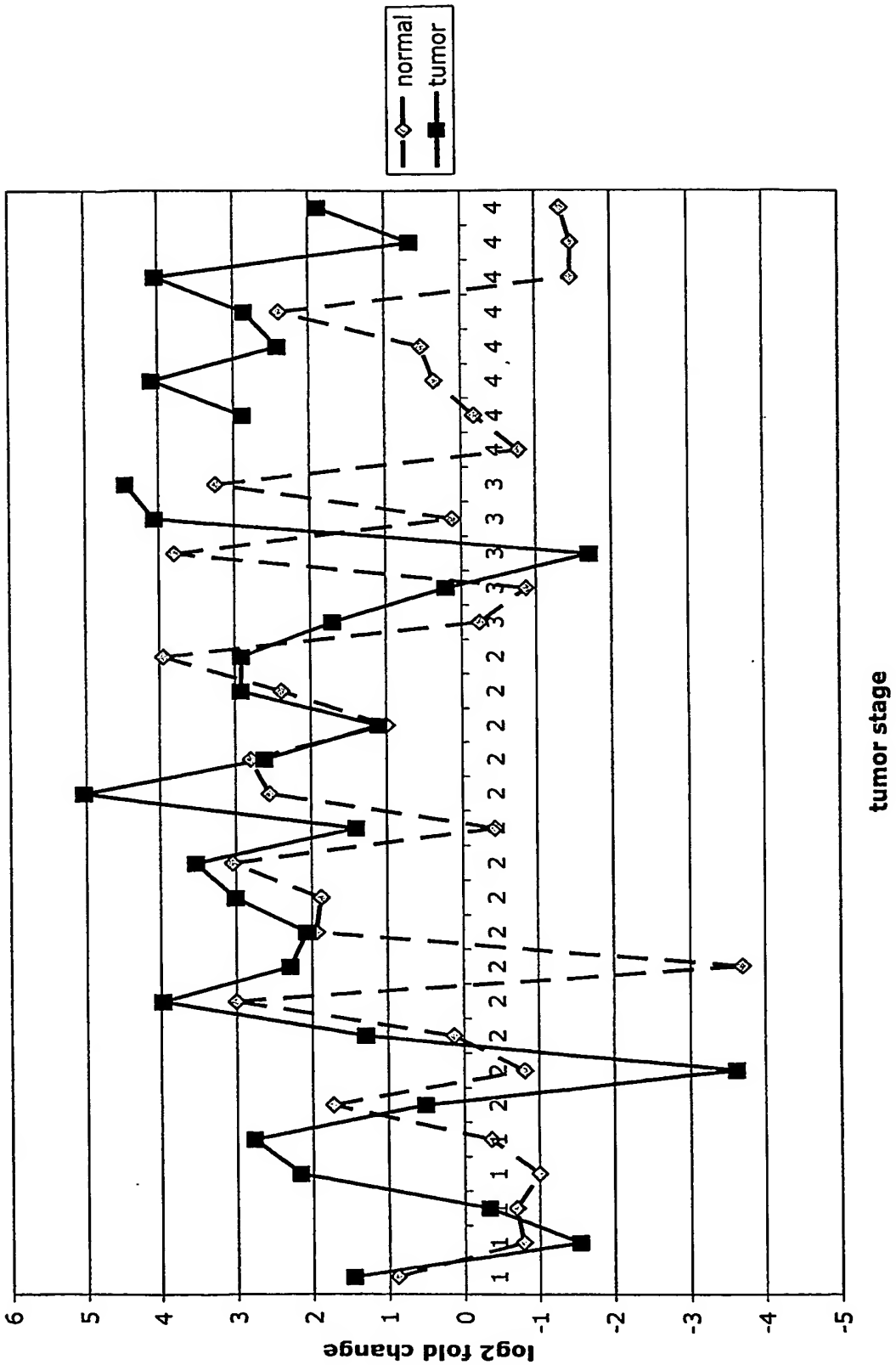


Fig. 10aa PCSK5

Fig. 10ab SERPINB5

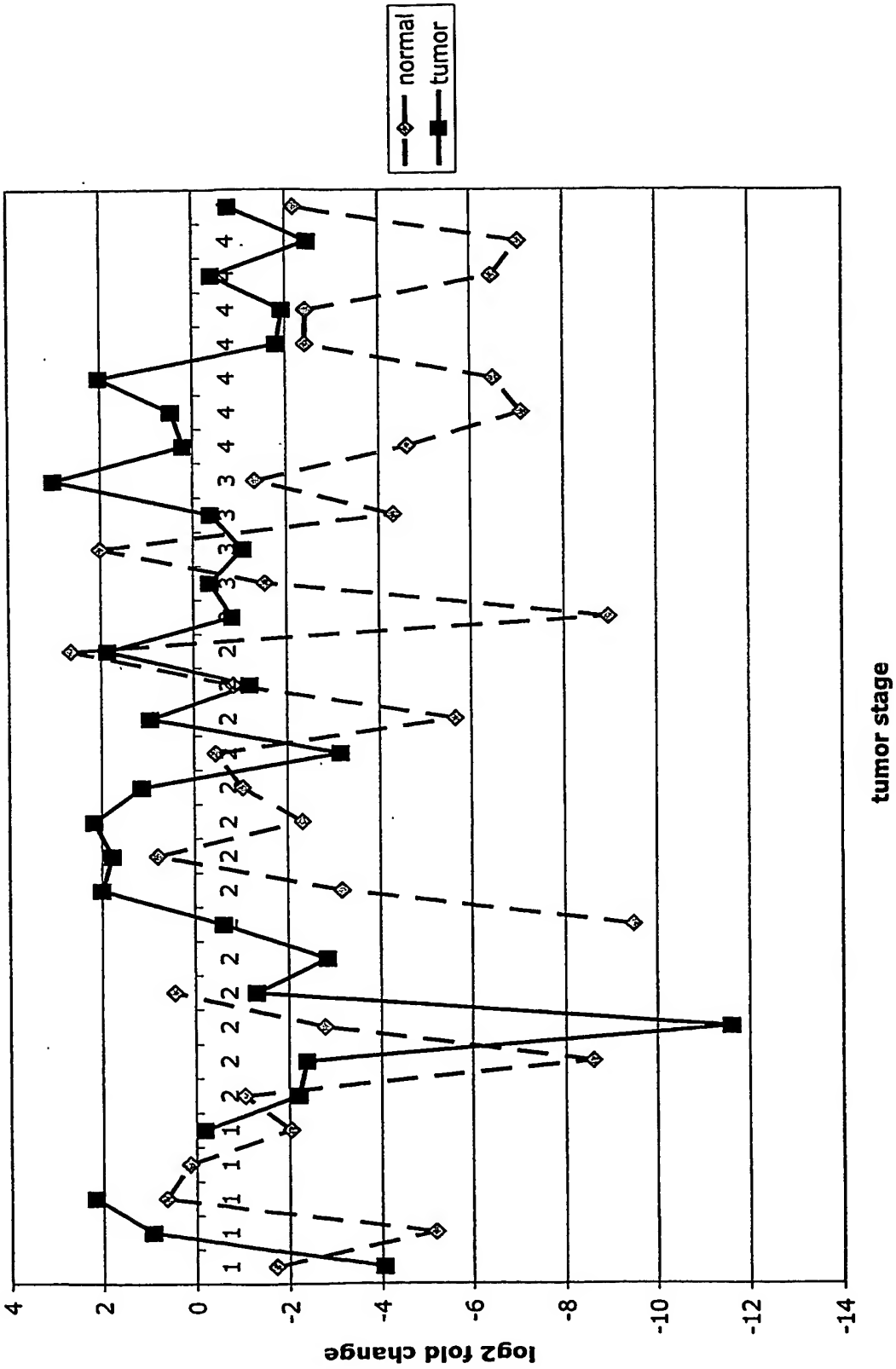
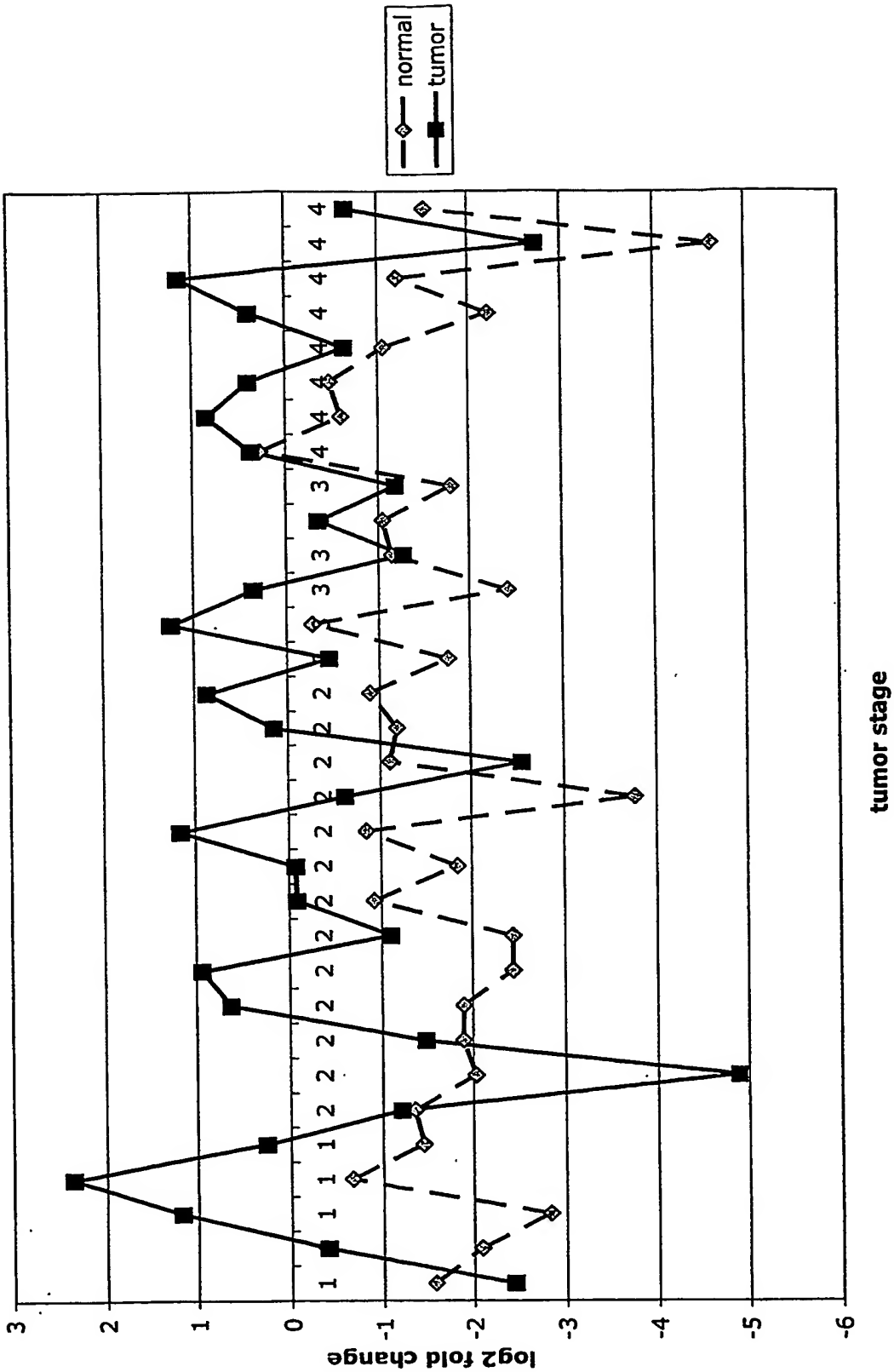
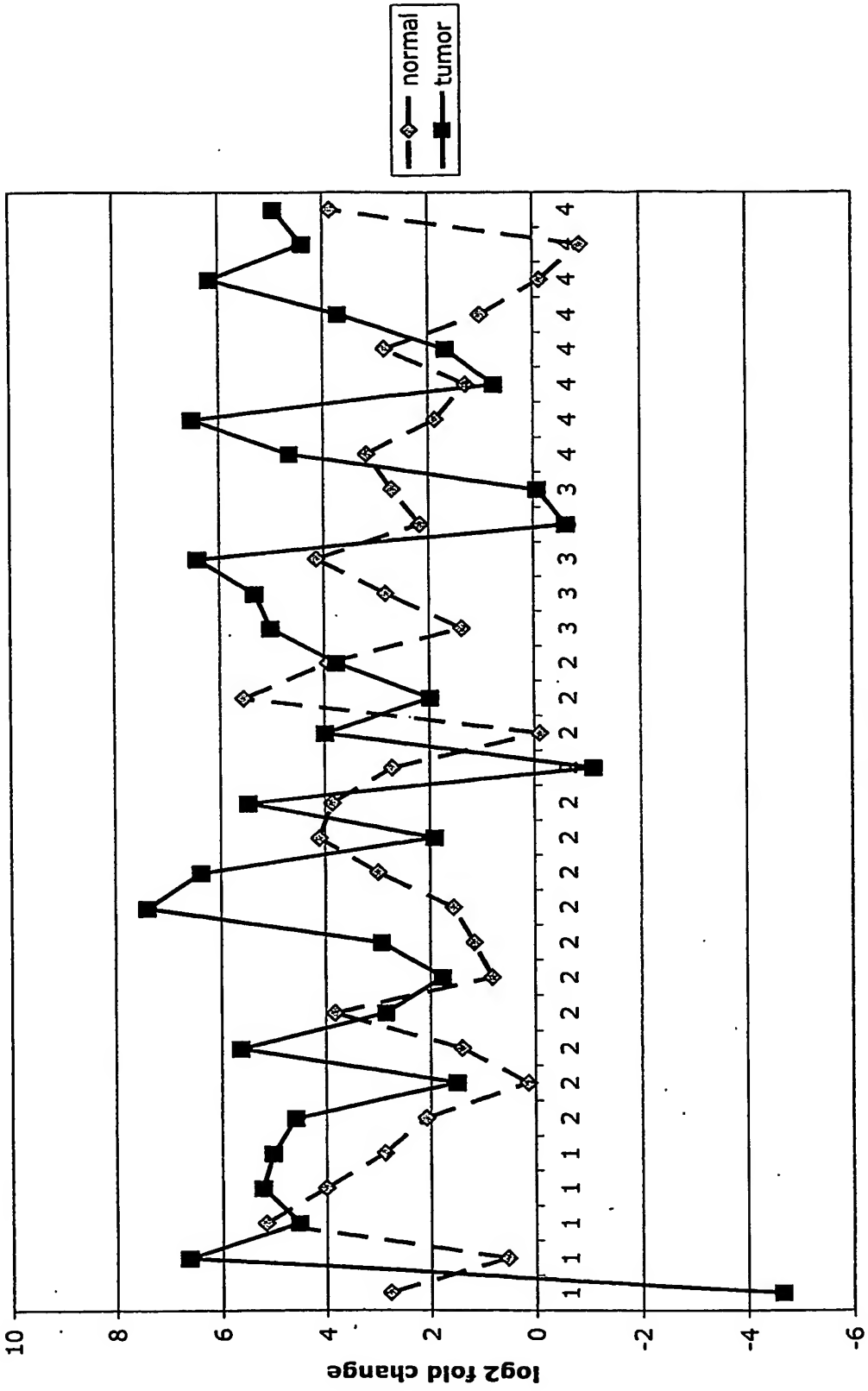


Fig. 10ac TGFb1

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tumor stage

Fig. 10ad CEA

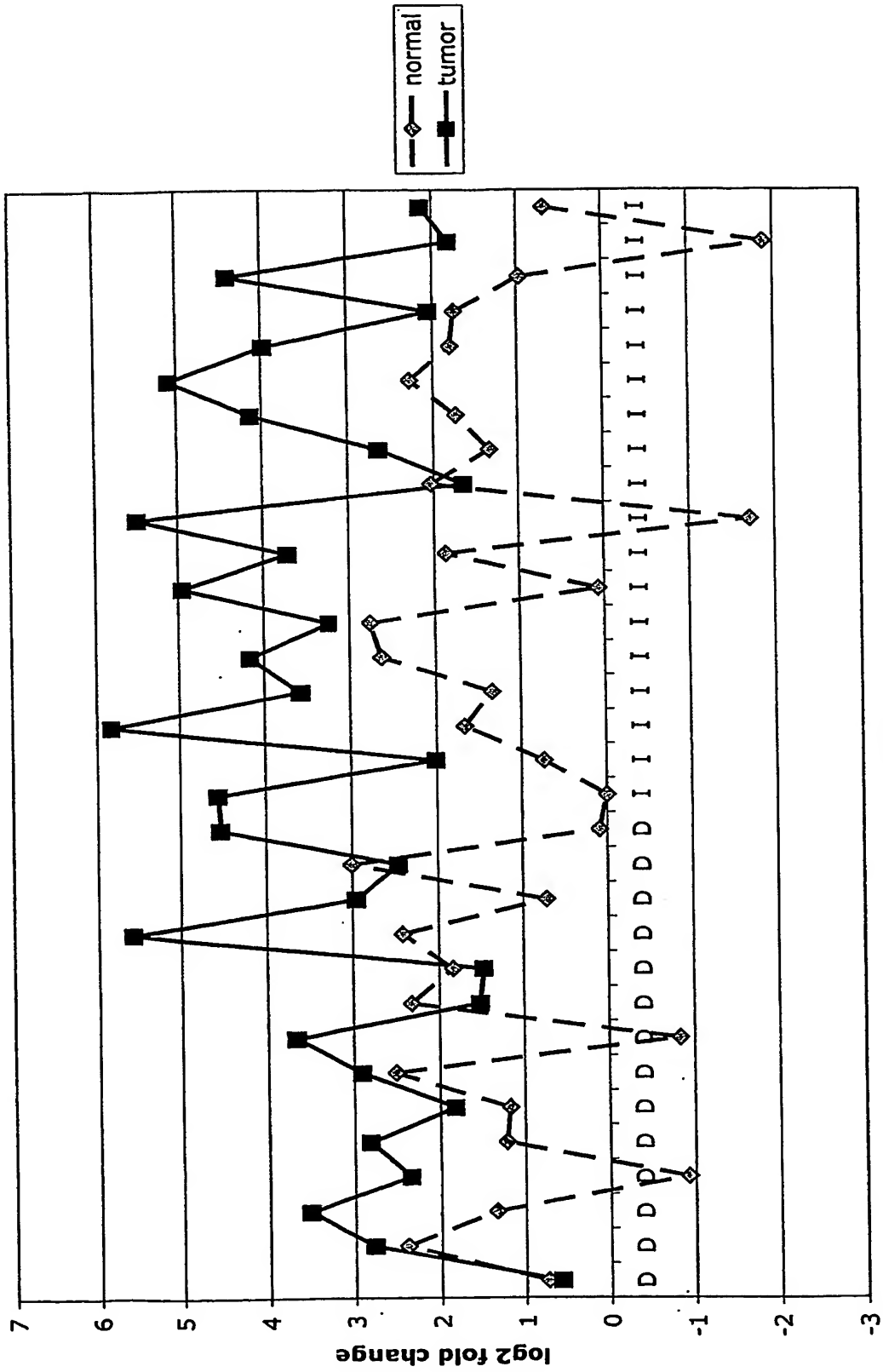


Fig. 11a Adlican

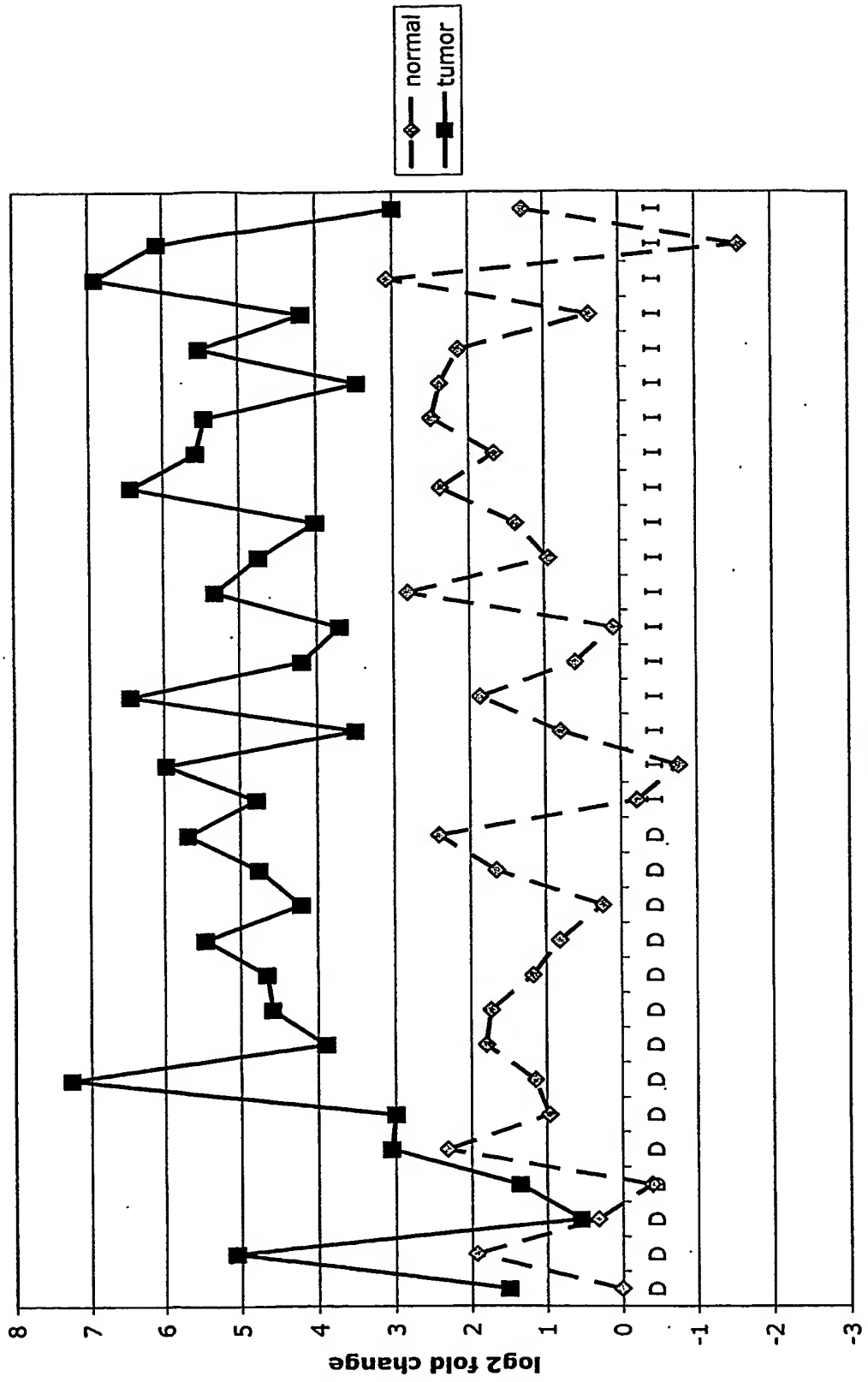
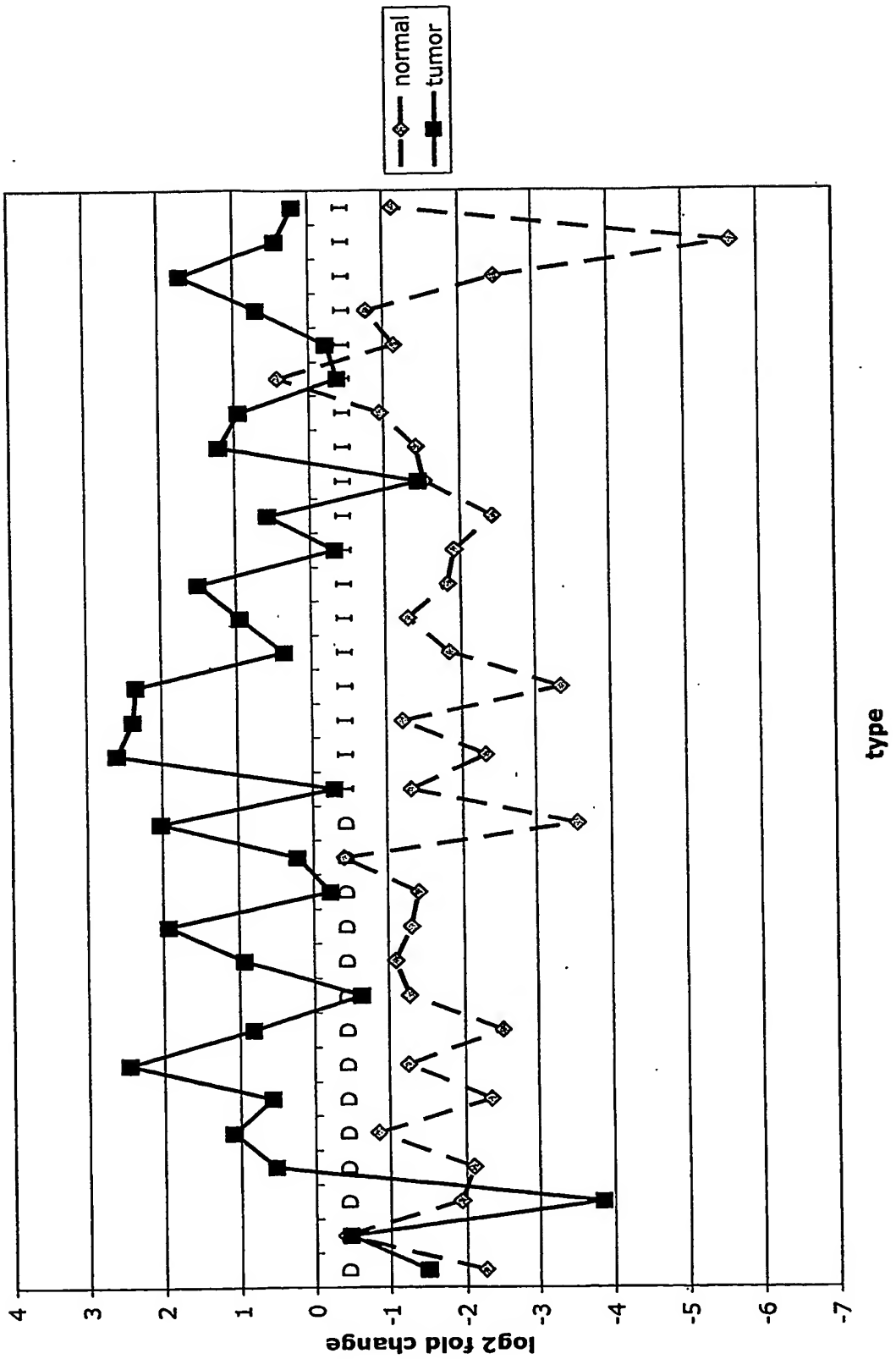


Fig. 11b ASPN

Fig. 11c CSPG2



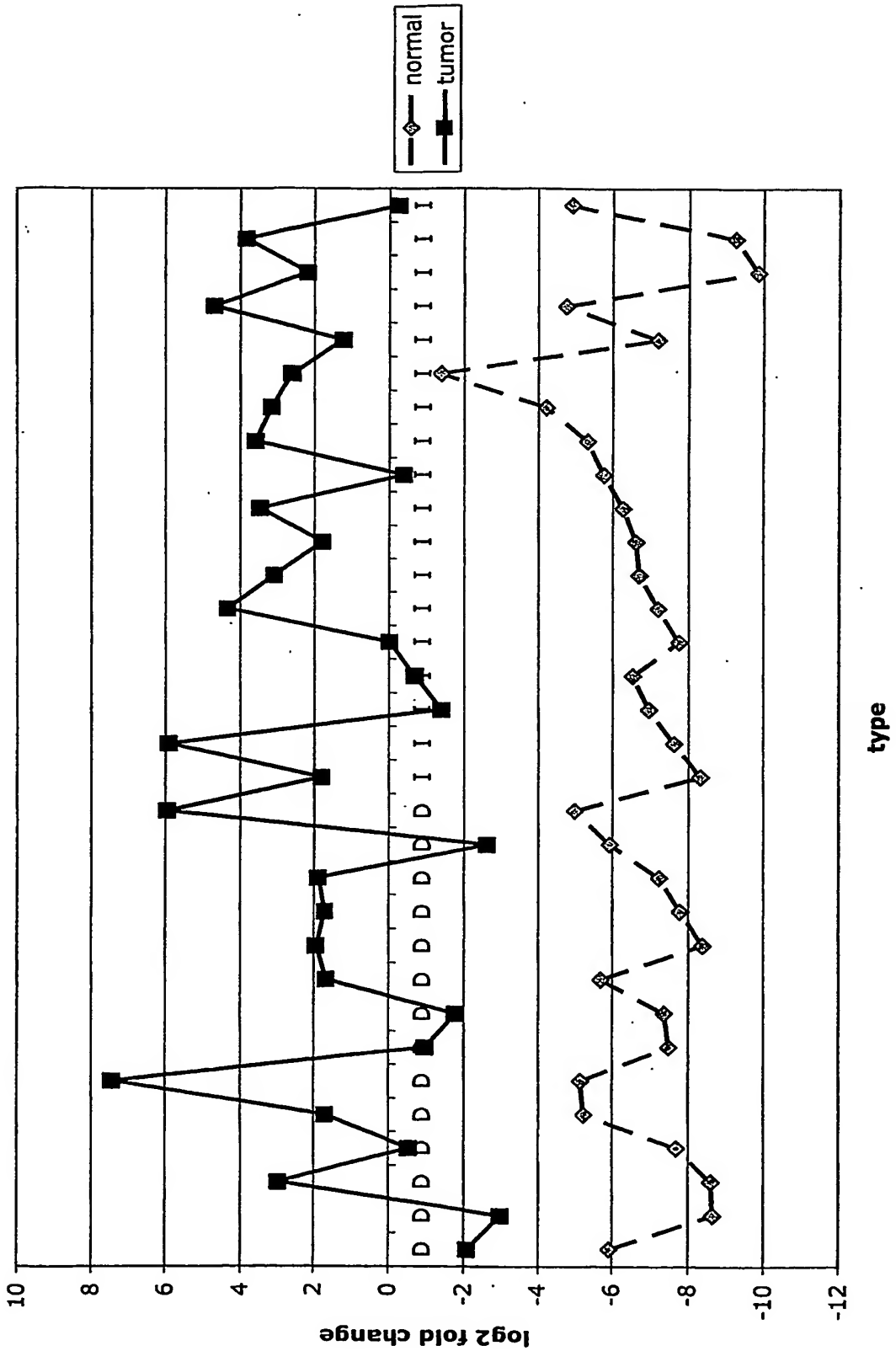
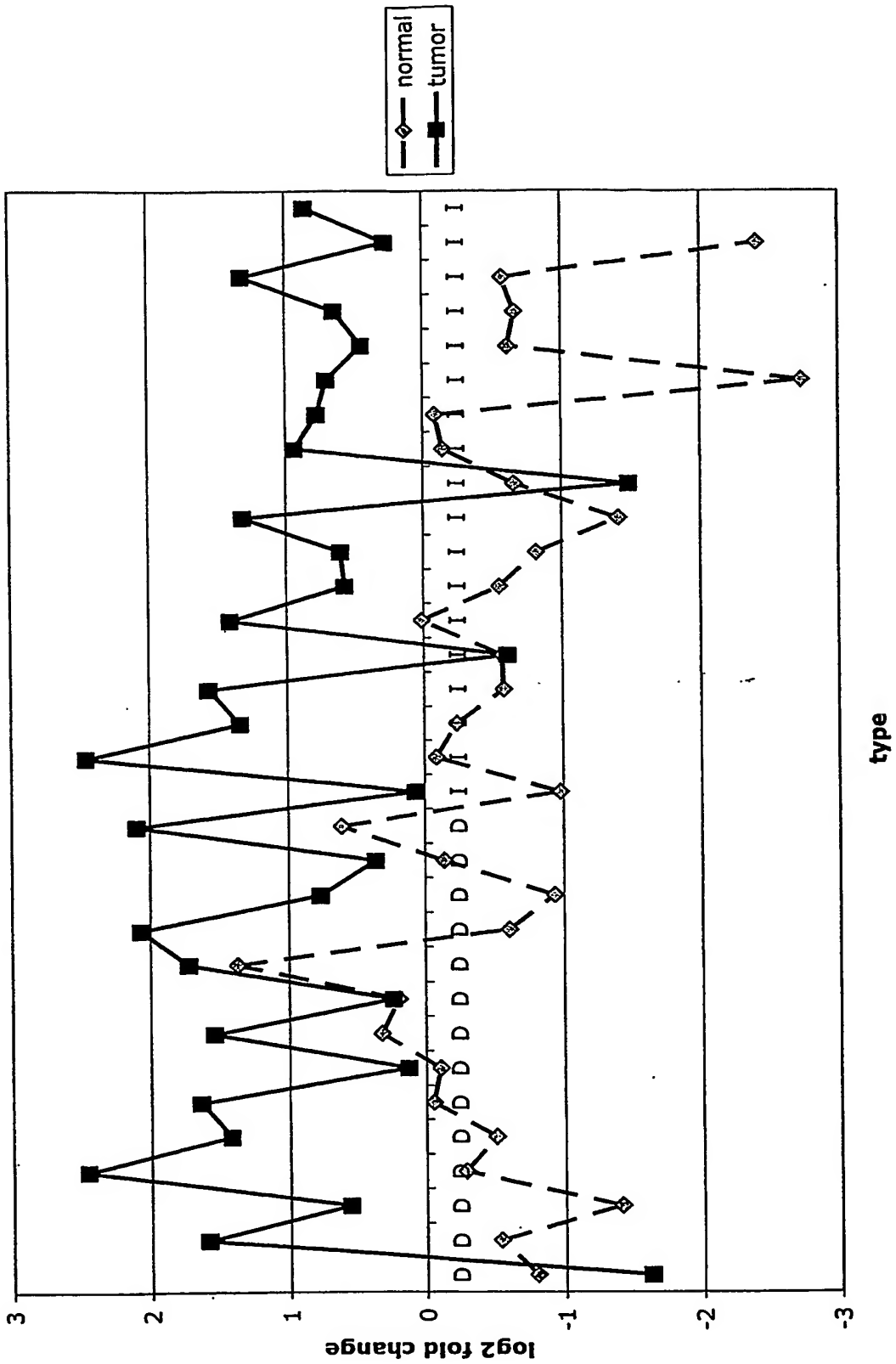


Fig. 11d CST1,2,4



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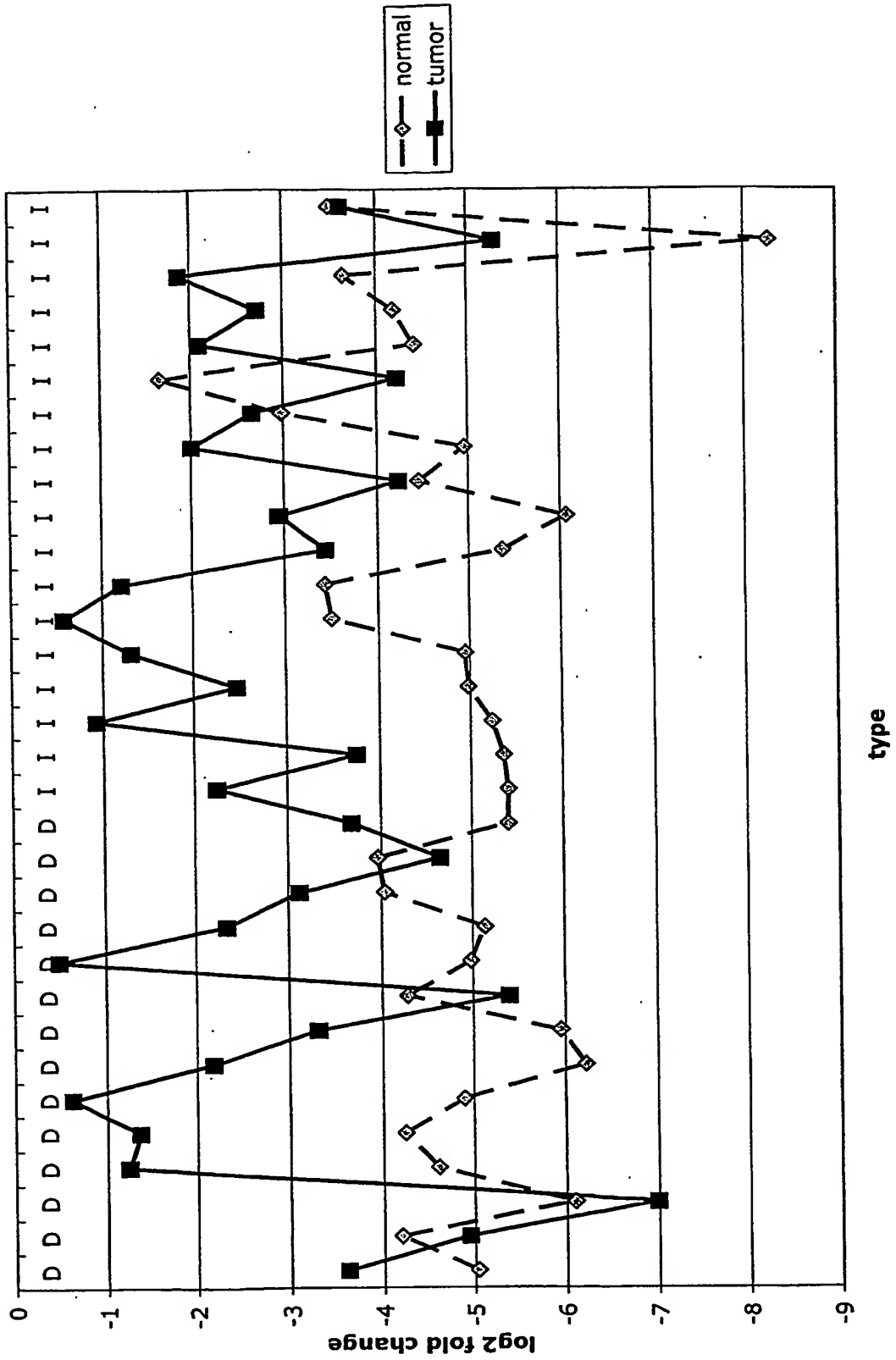


Fig. 11f GGH

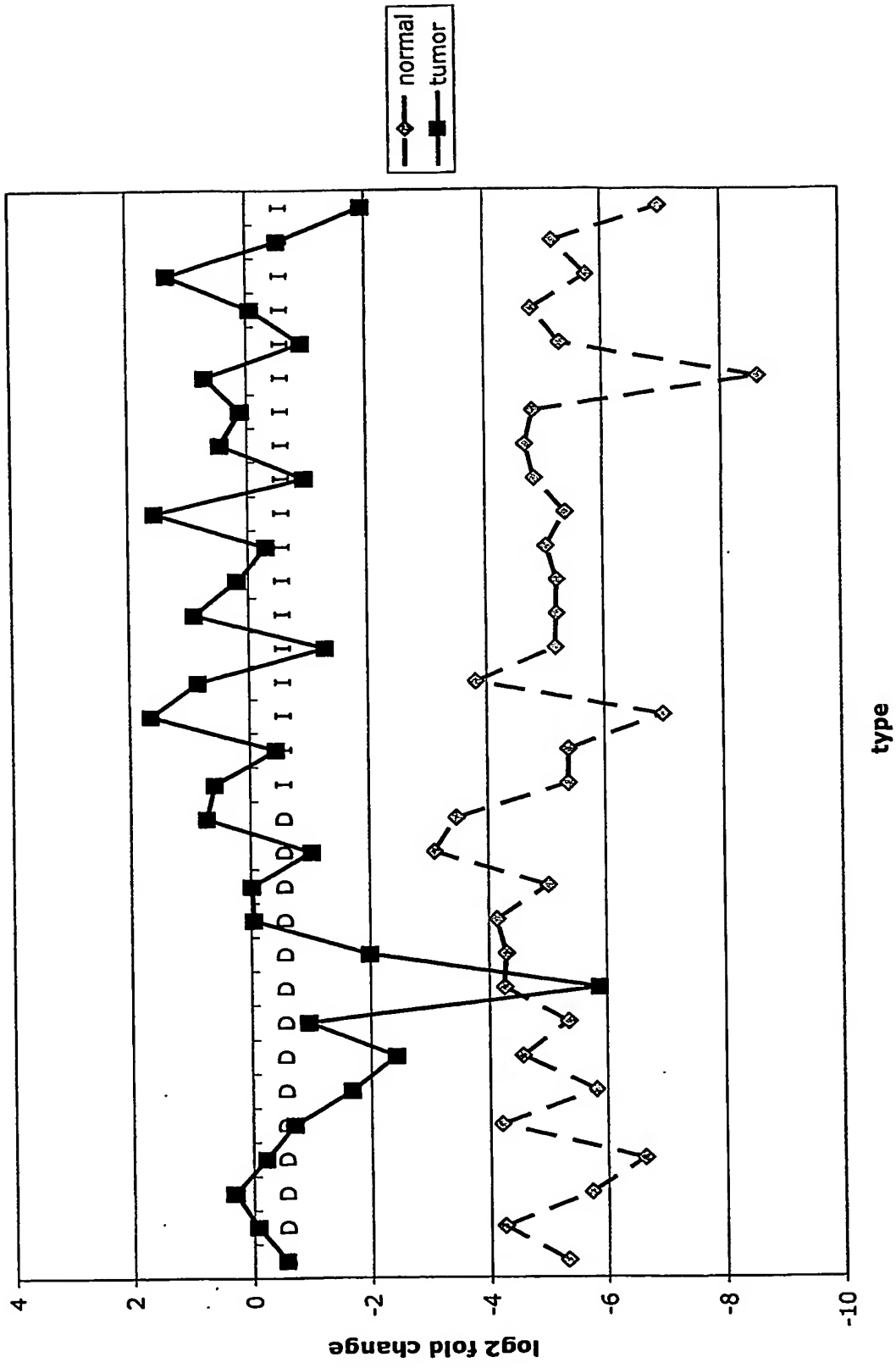
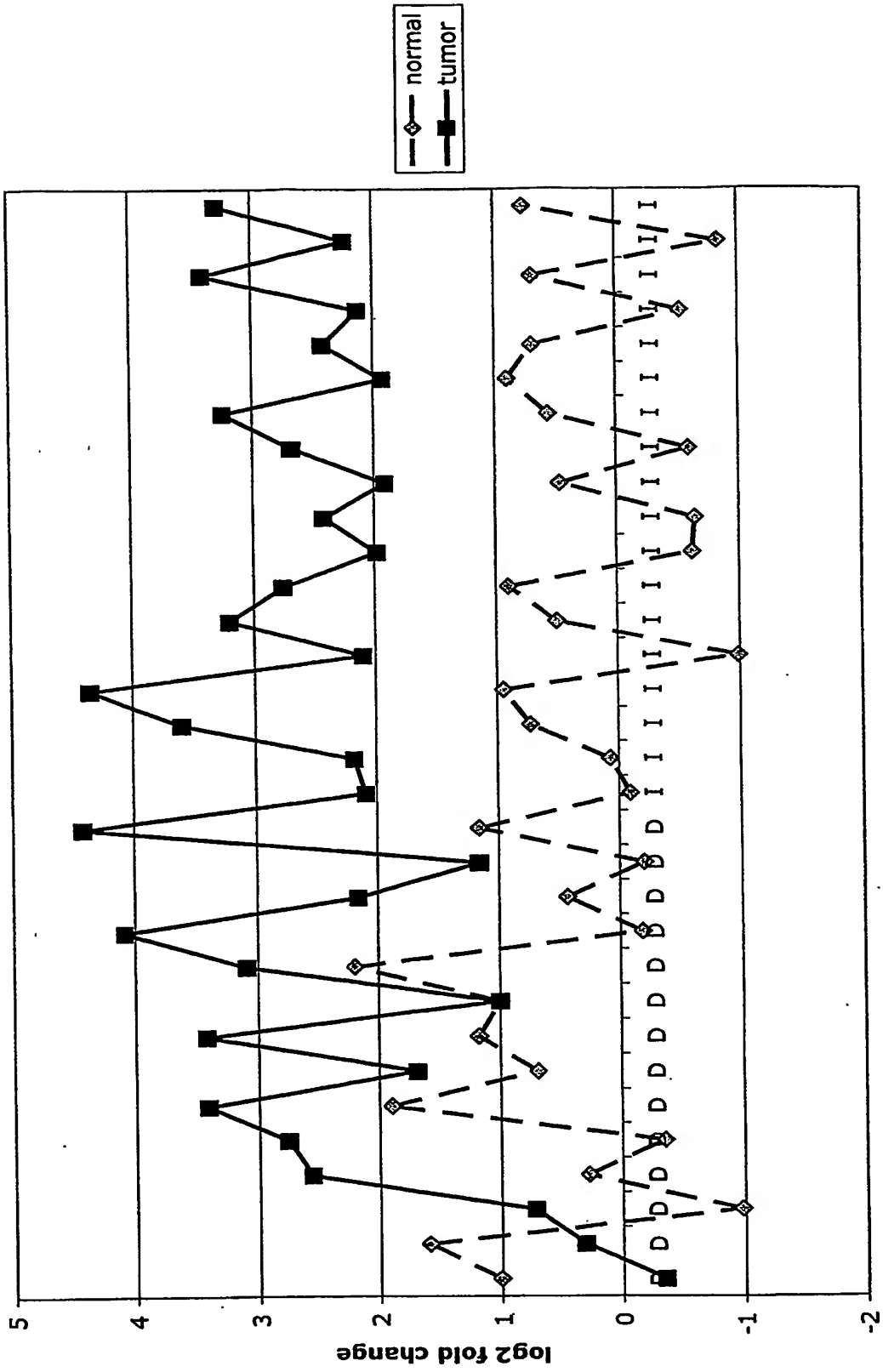


Fig. 11g INHBA



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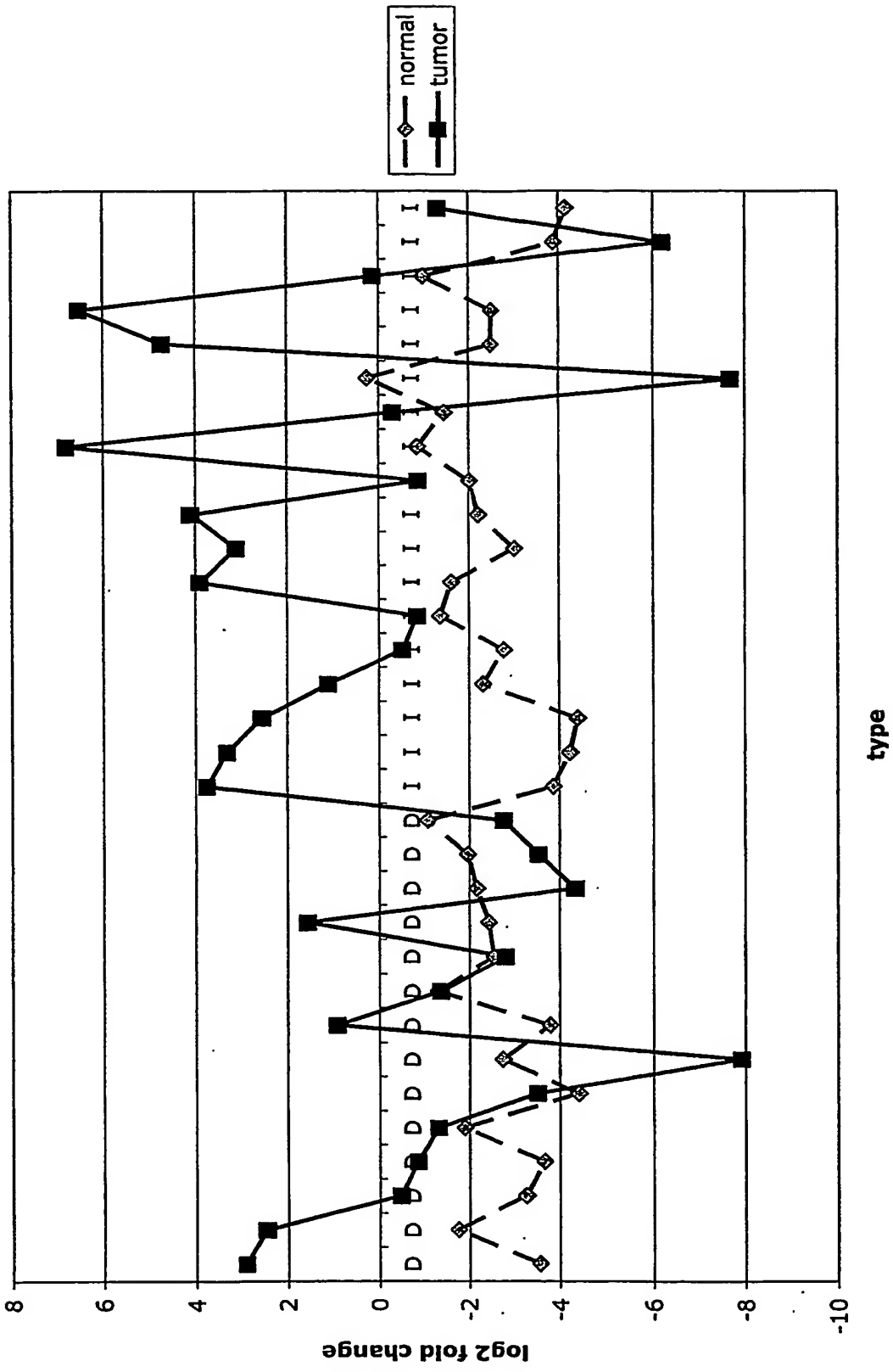

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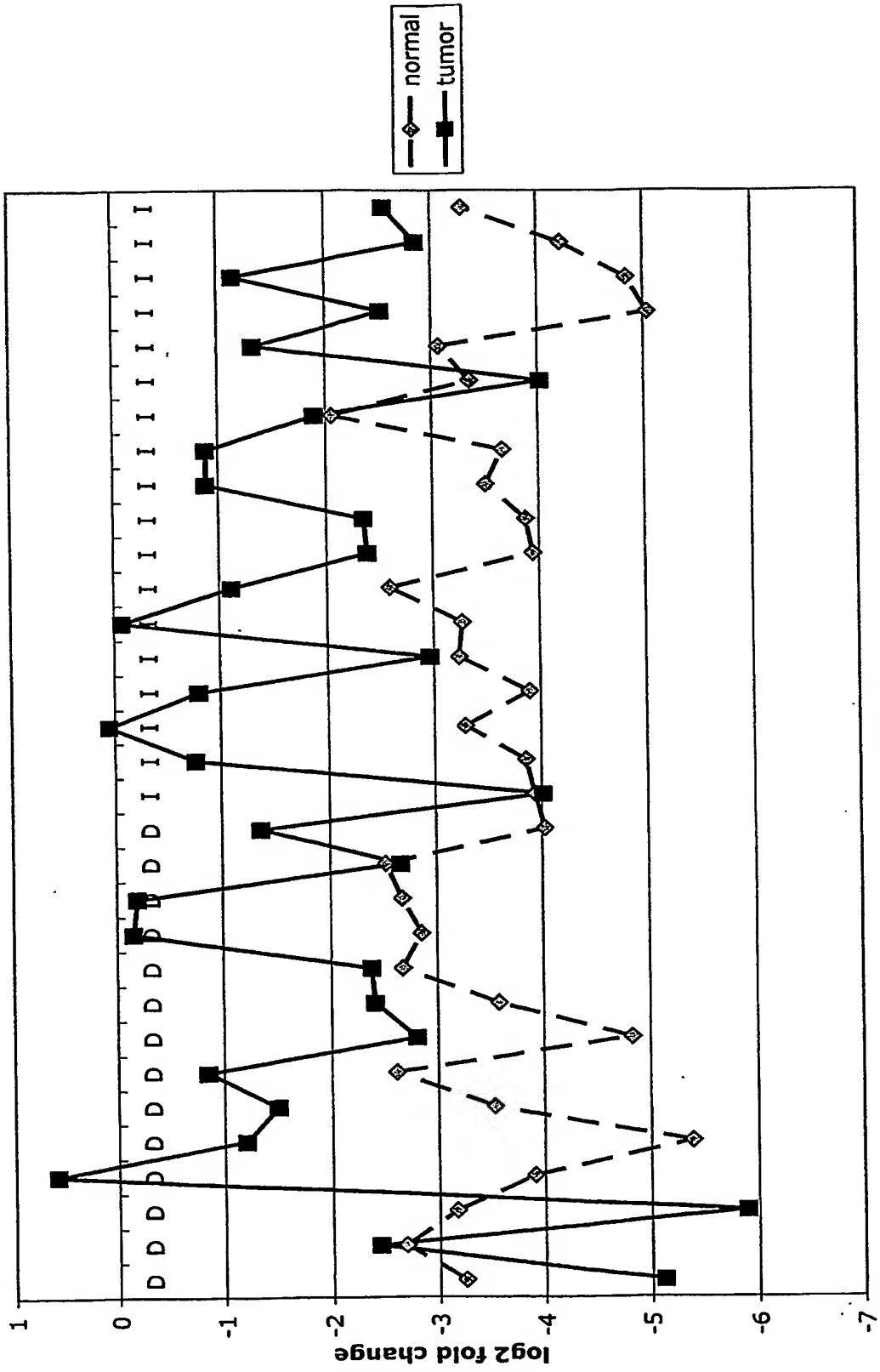
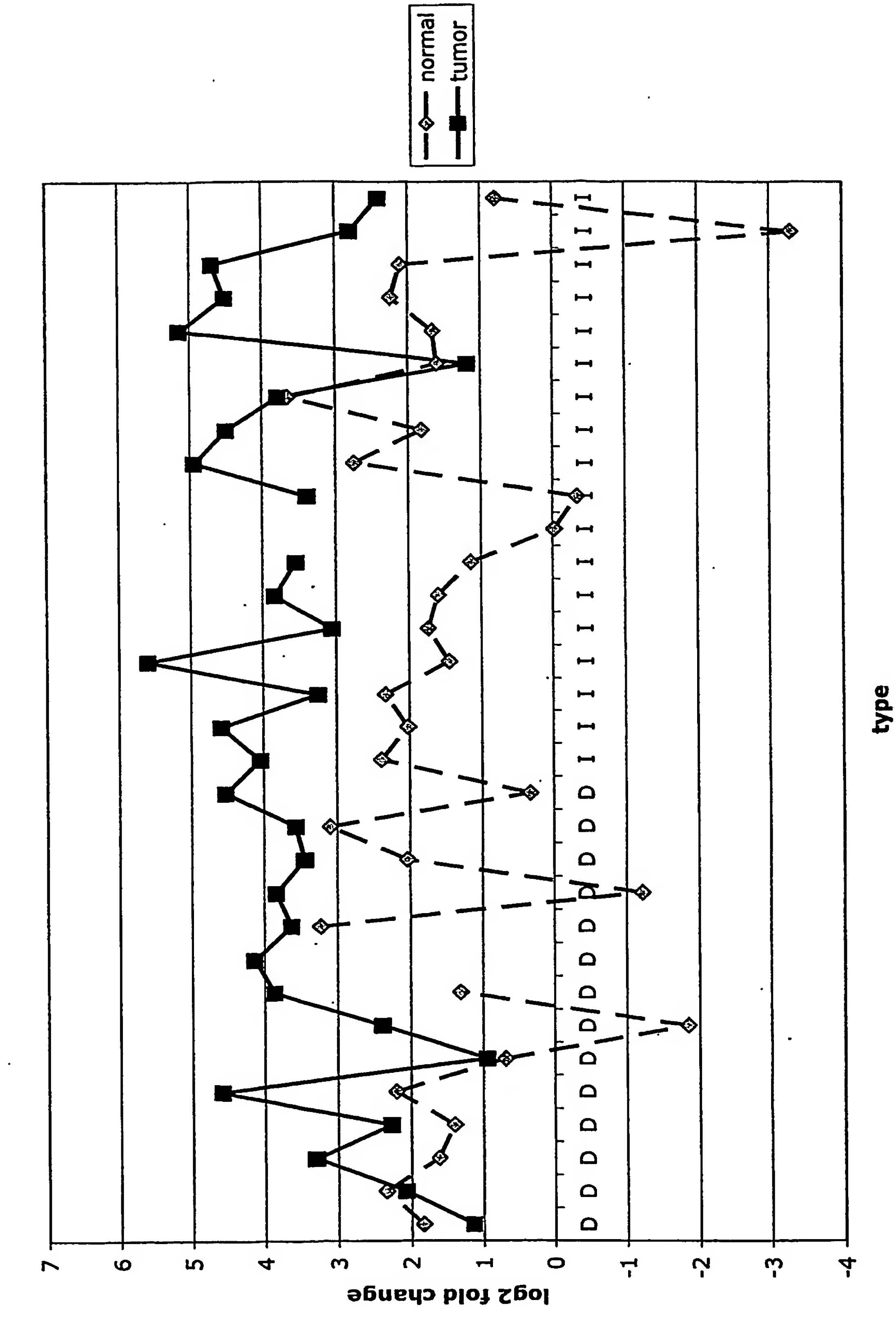


Fig. 11j LEPRE1

Fig. 11k LUM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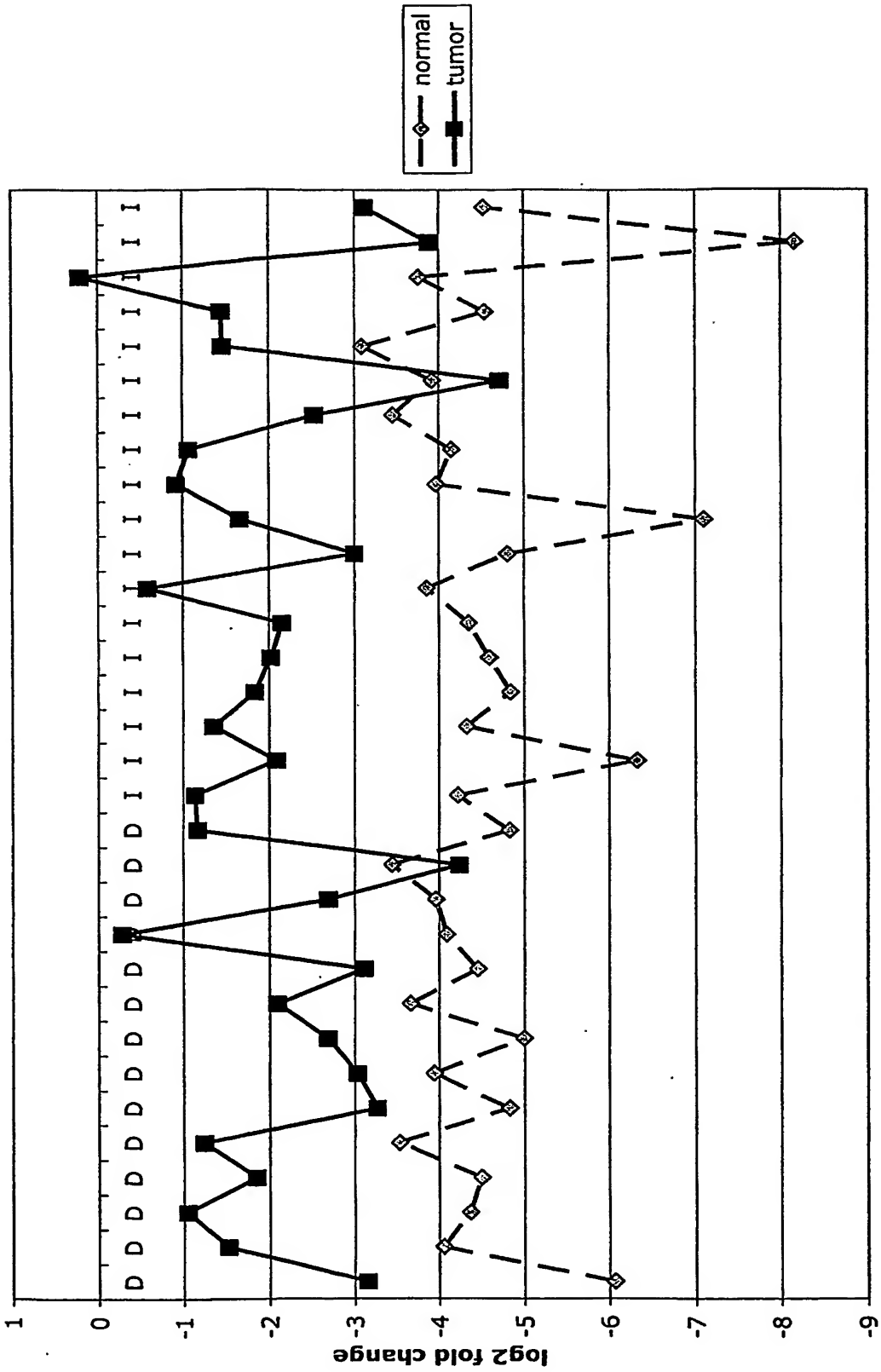


Fig. 11l LOXL2

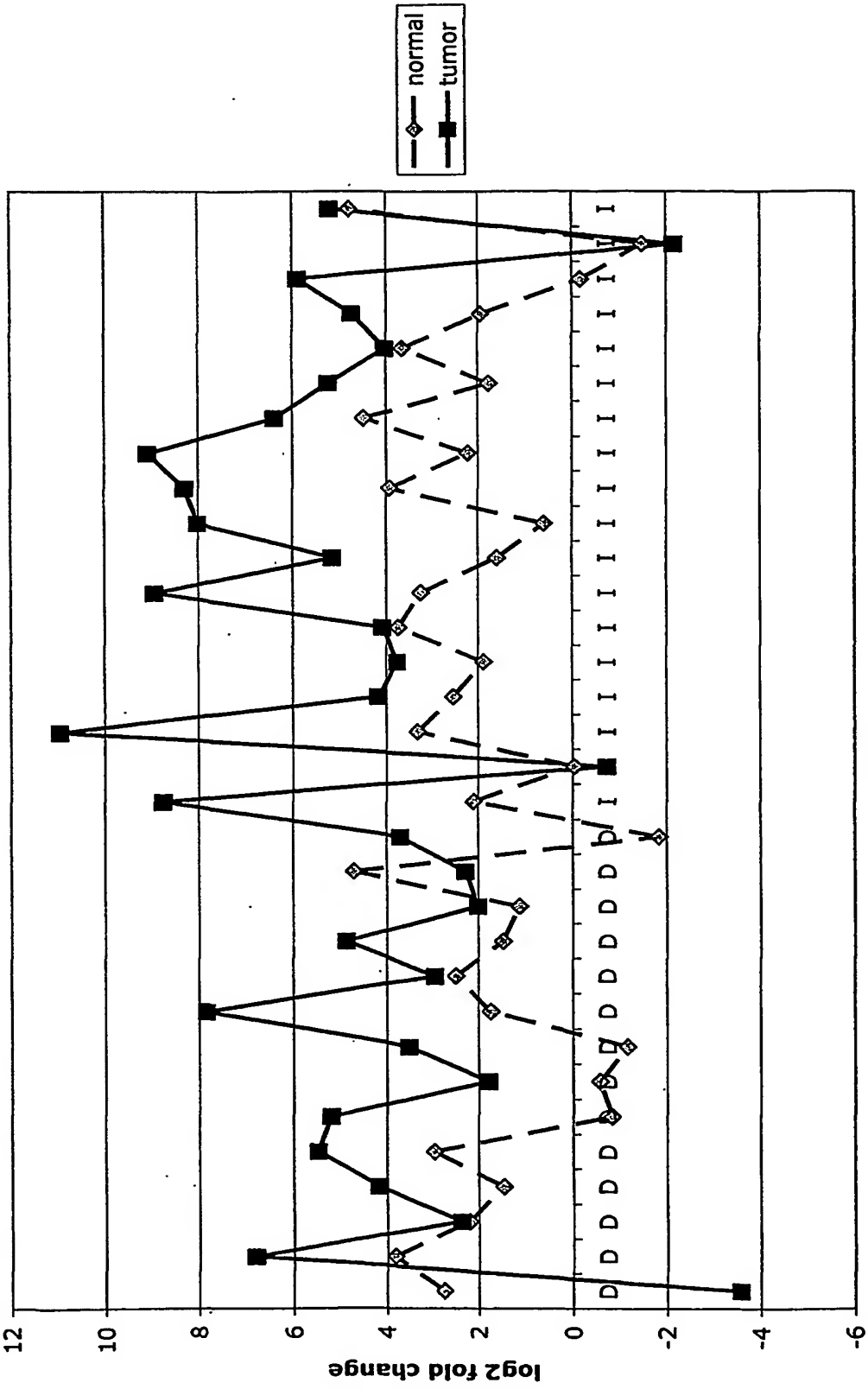


Fig. 11m MMP12

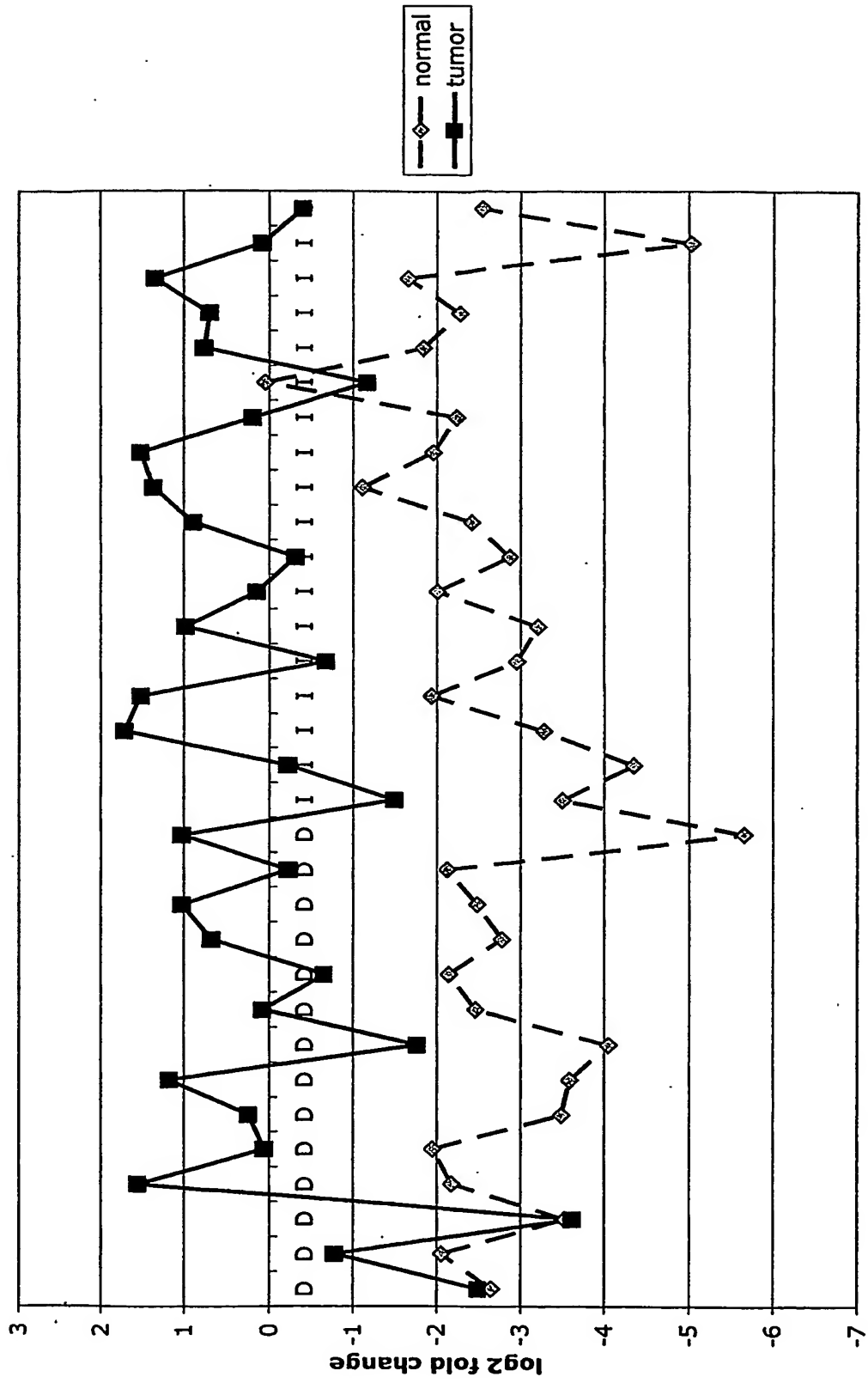


Fig. 11n TIMP1

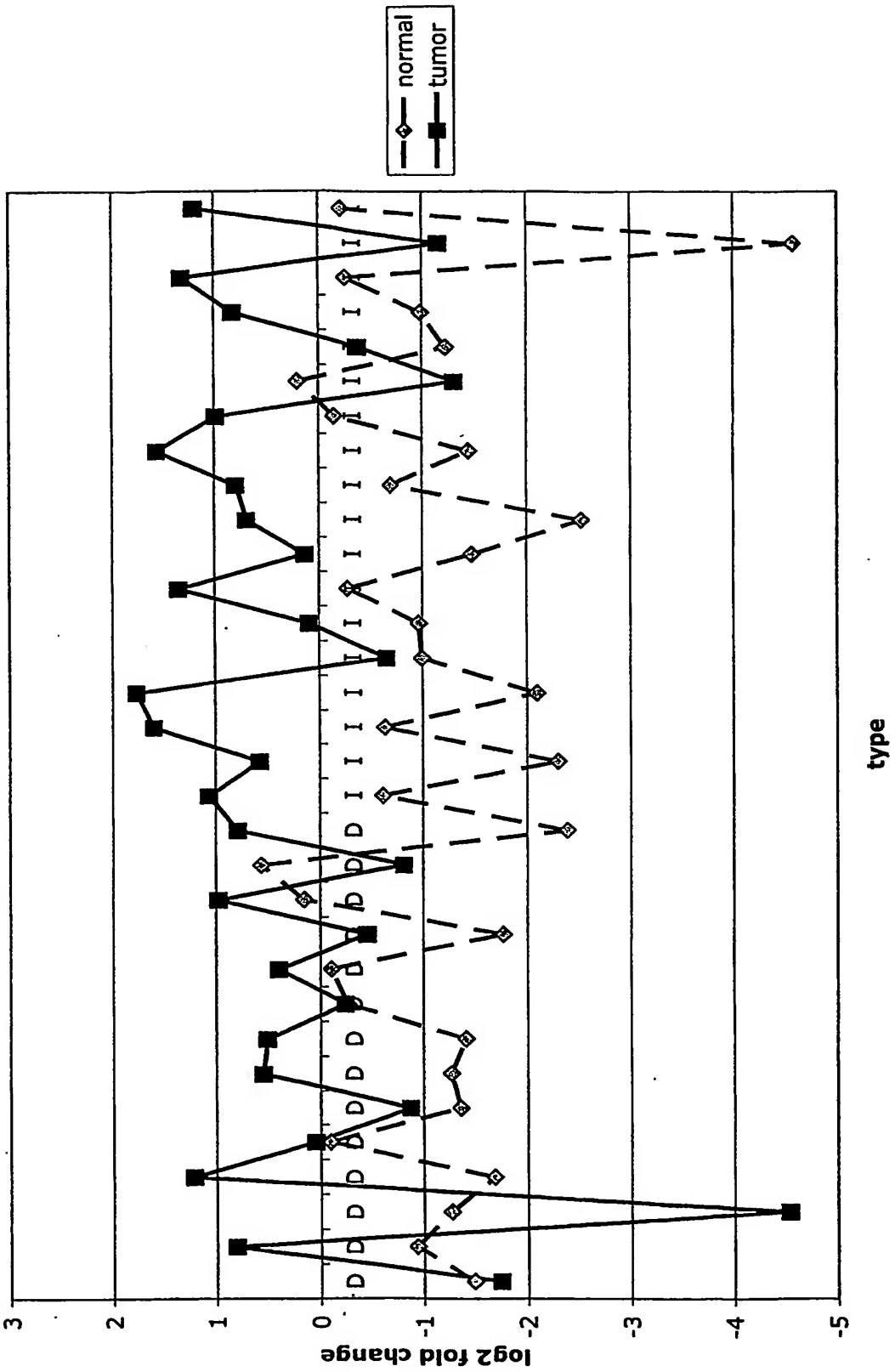


Fig. 11o ASAH1

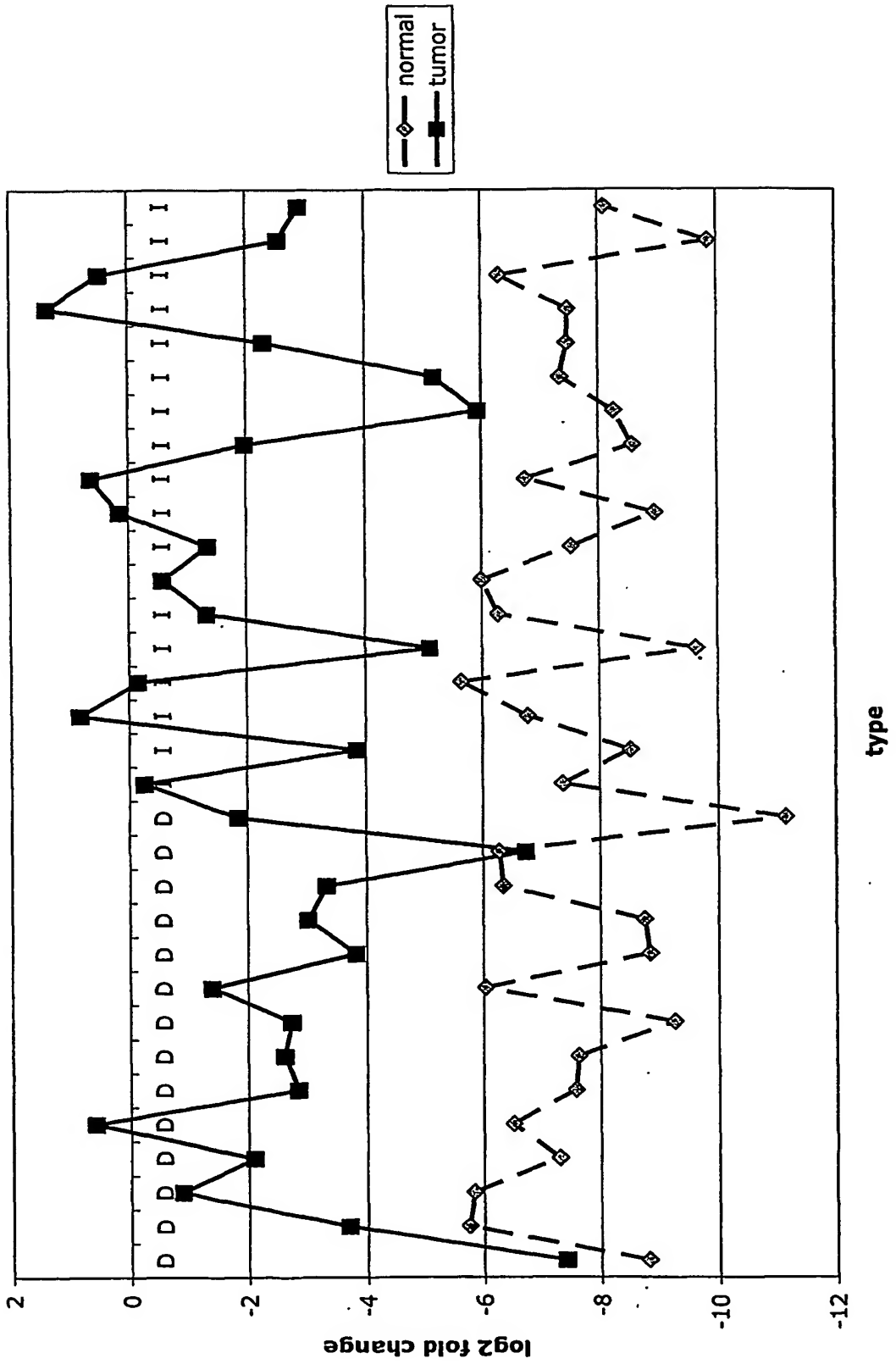


Fig. 11p SPP1

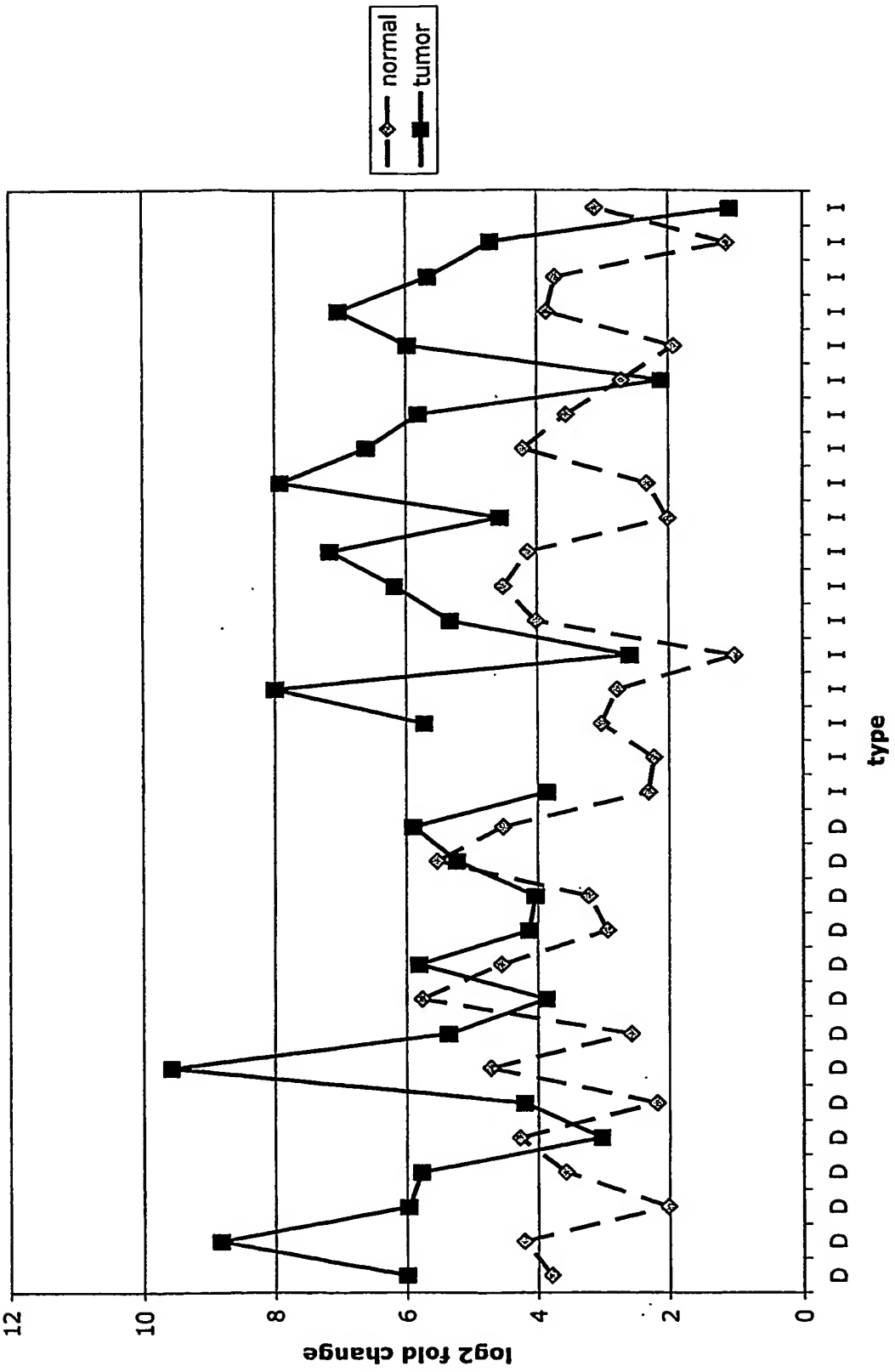


Fig. 11q SFRP2

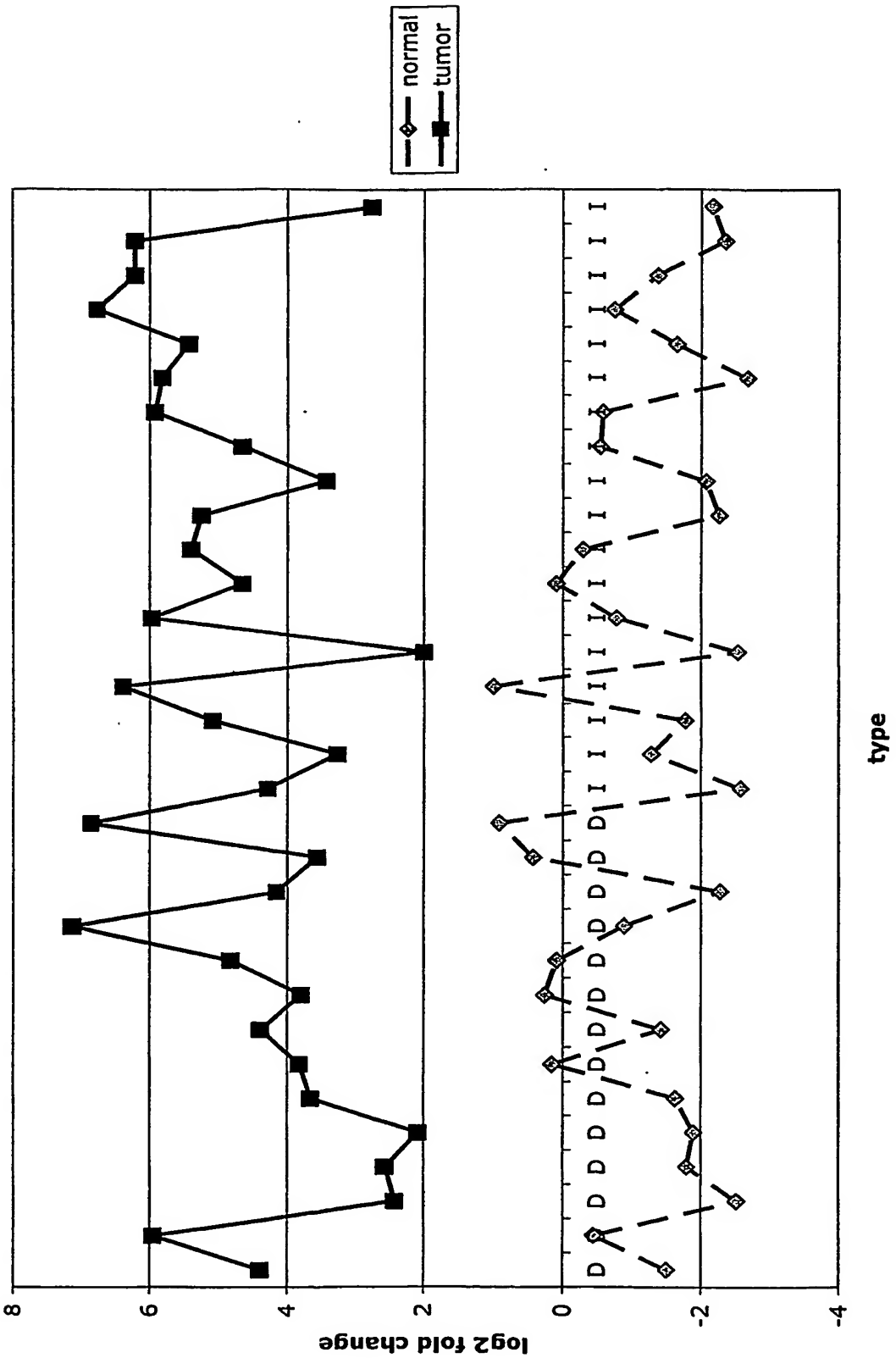


Fig. 11r SFRP4

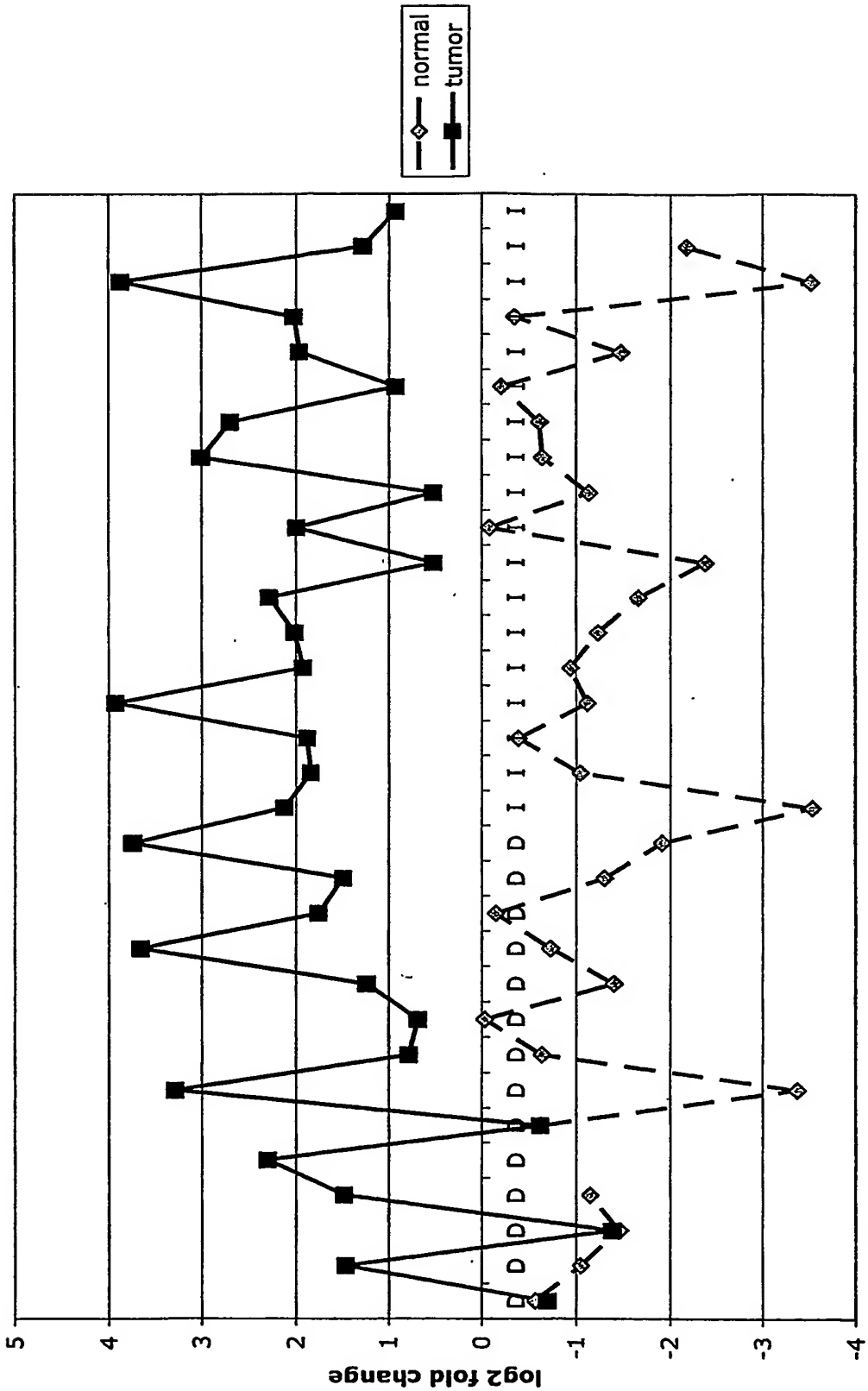


Fig. 11s SPARC

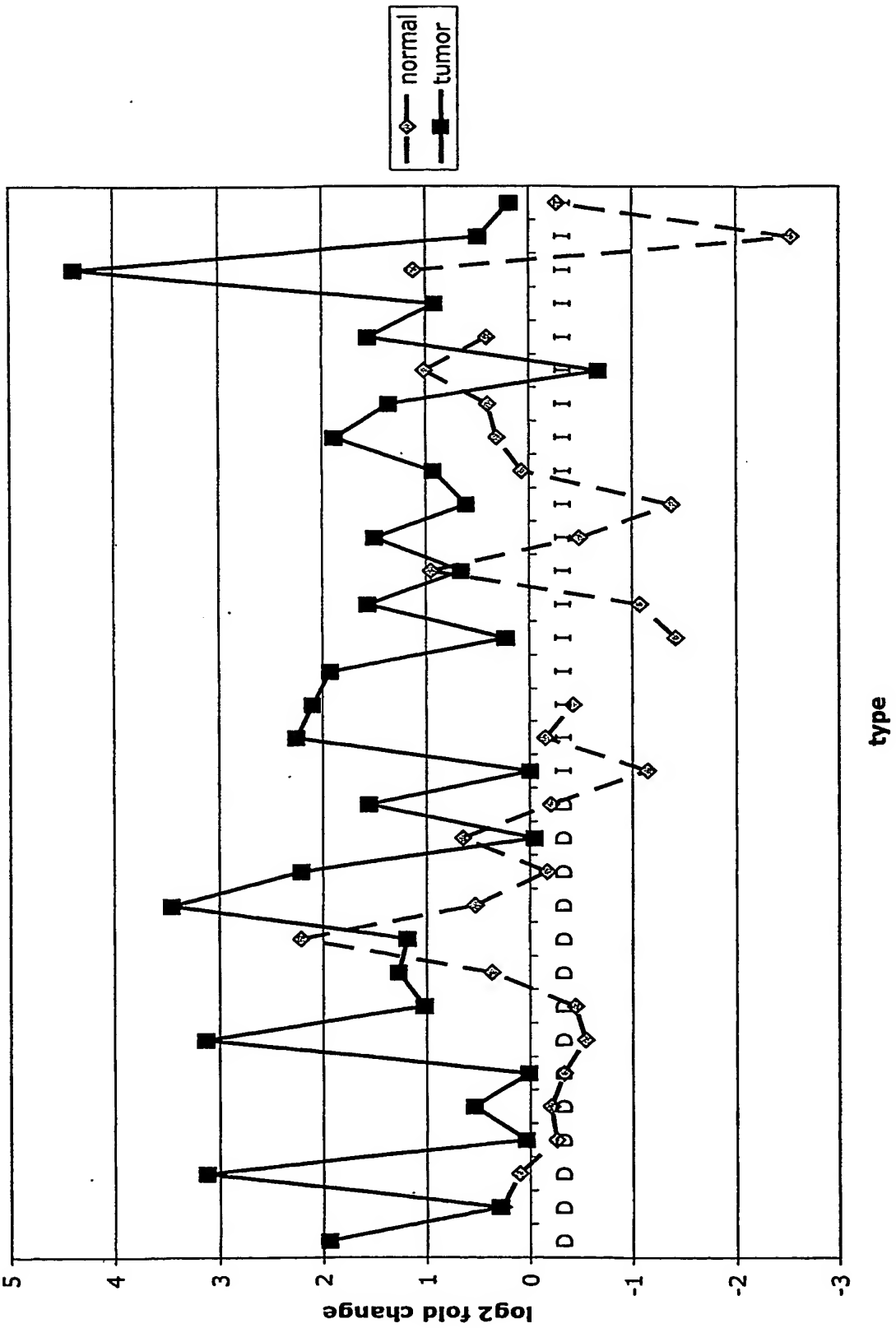


Fig. 11t PRSS11

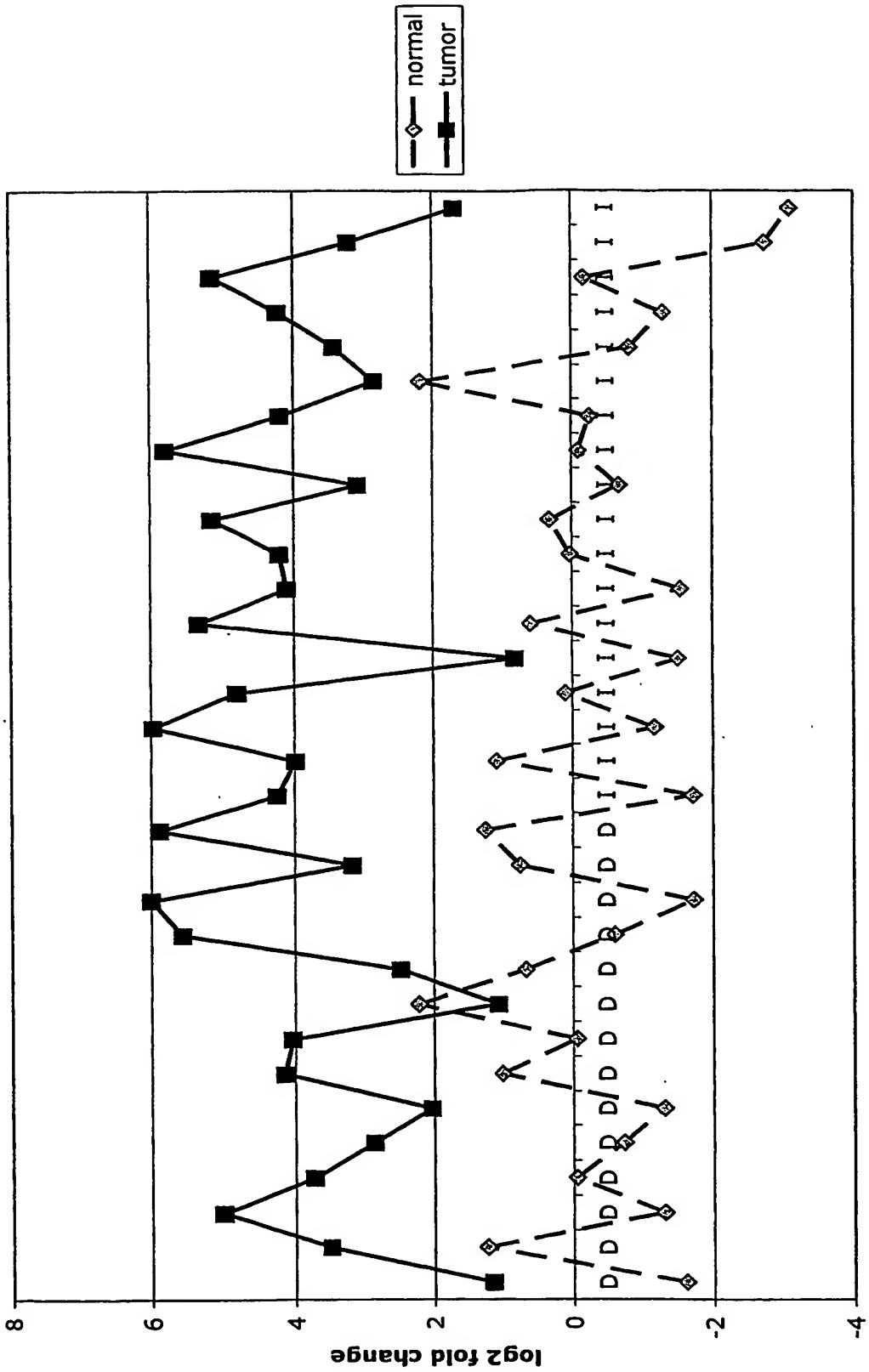


Fig. 11u THBS2

Fig. 11v TG

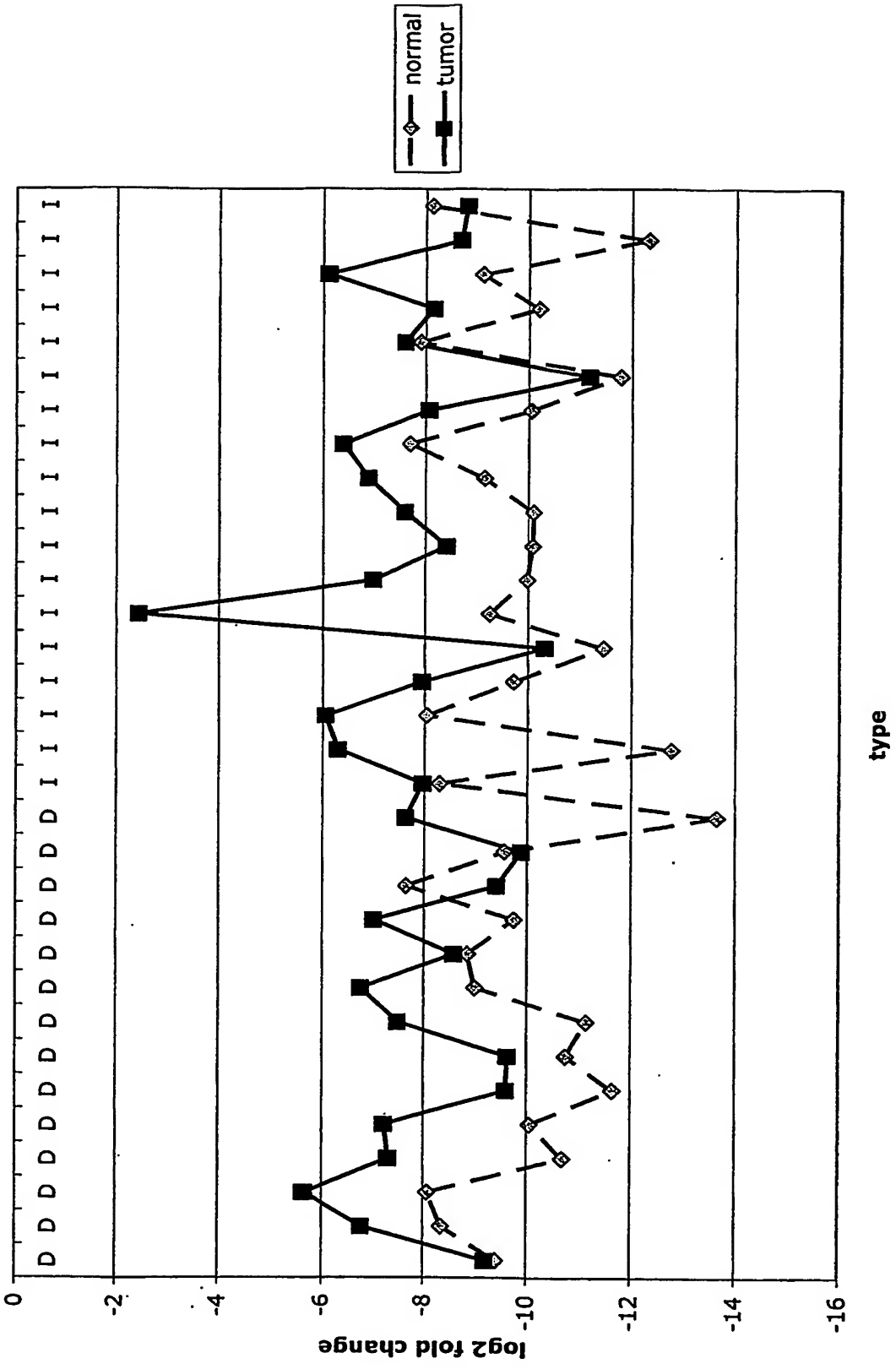


Fig. 11w TGFBI

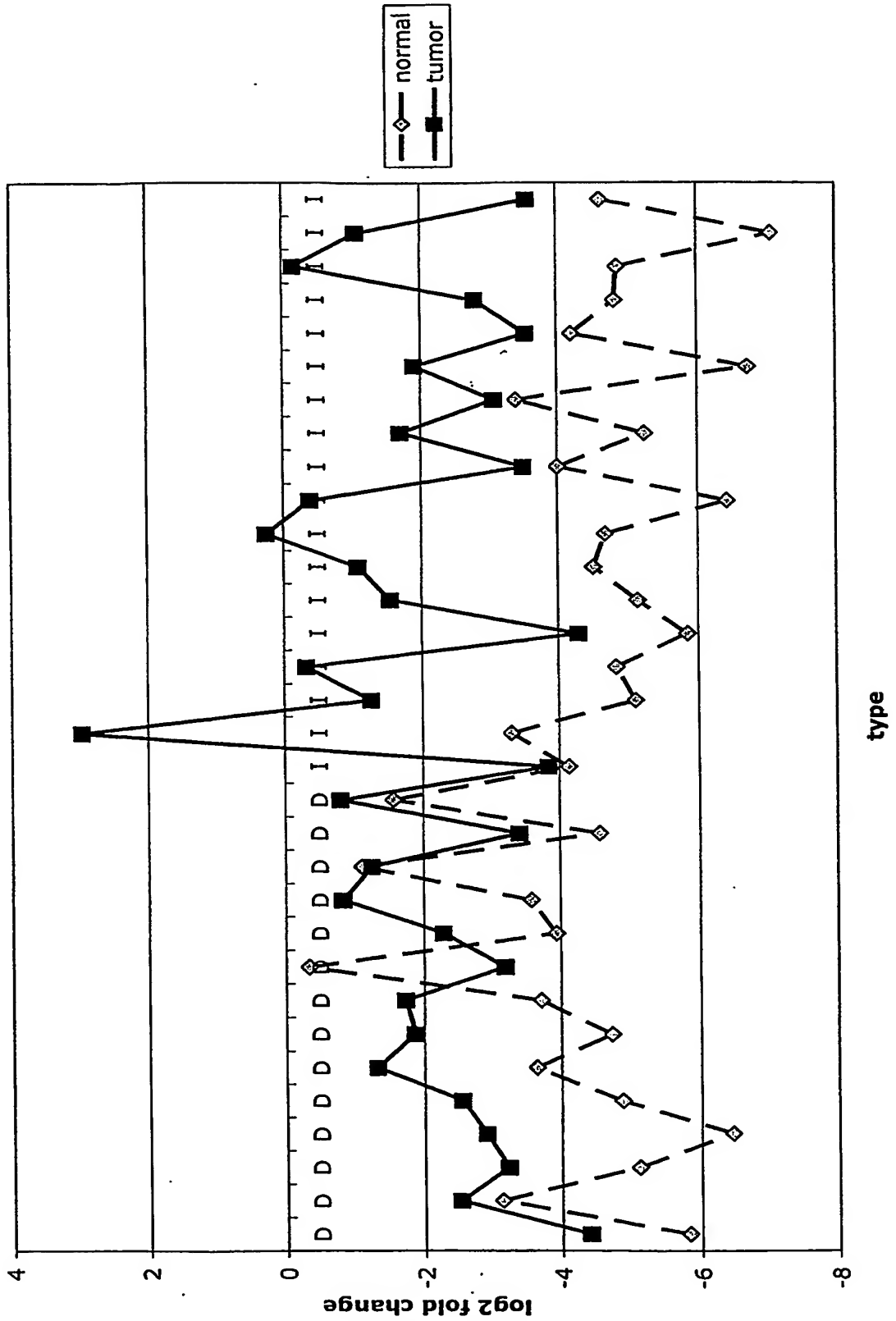


Fig. 11x CGR11

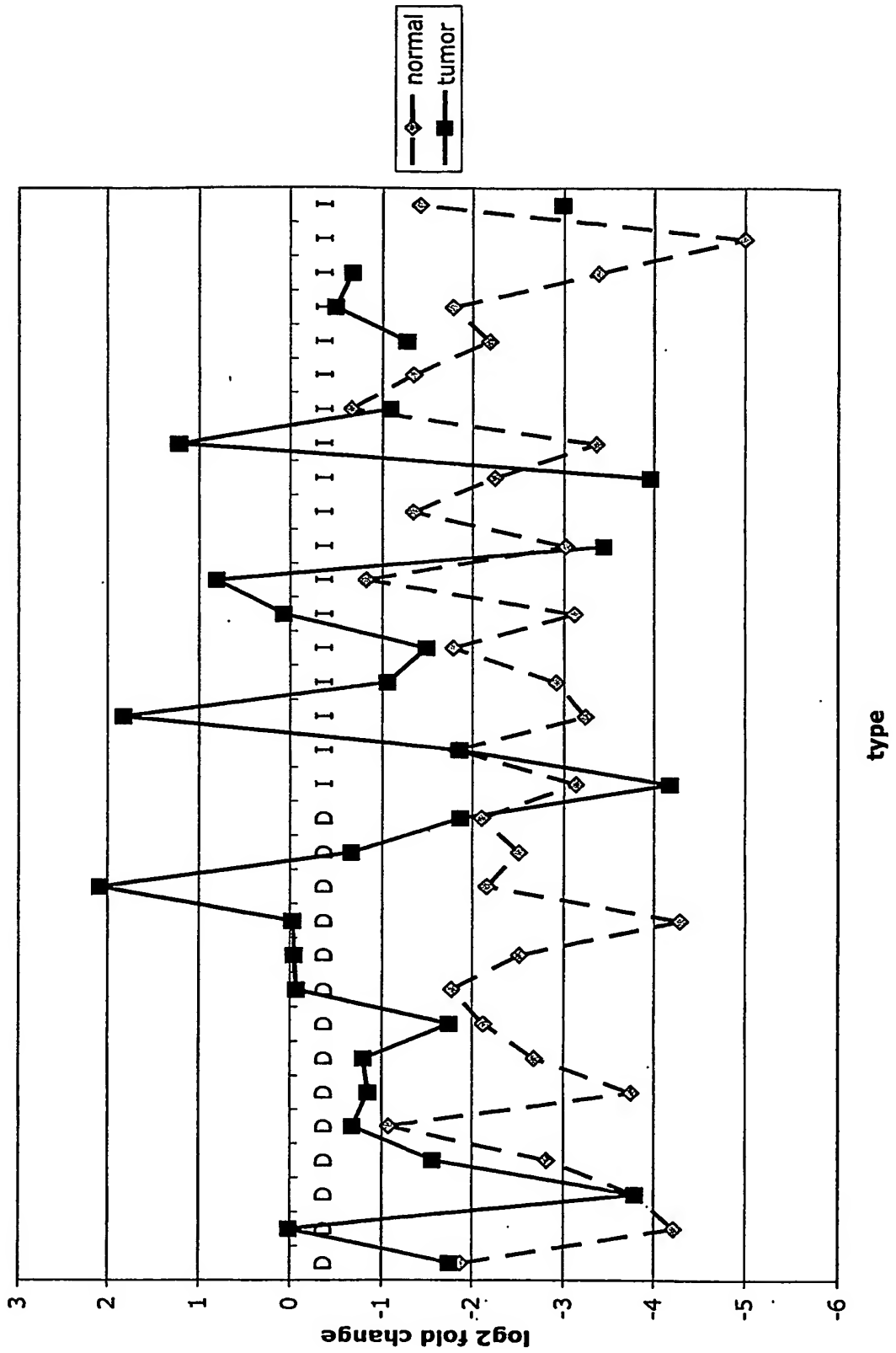
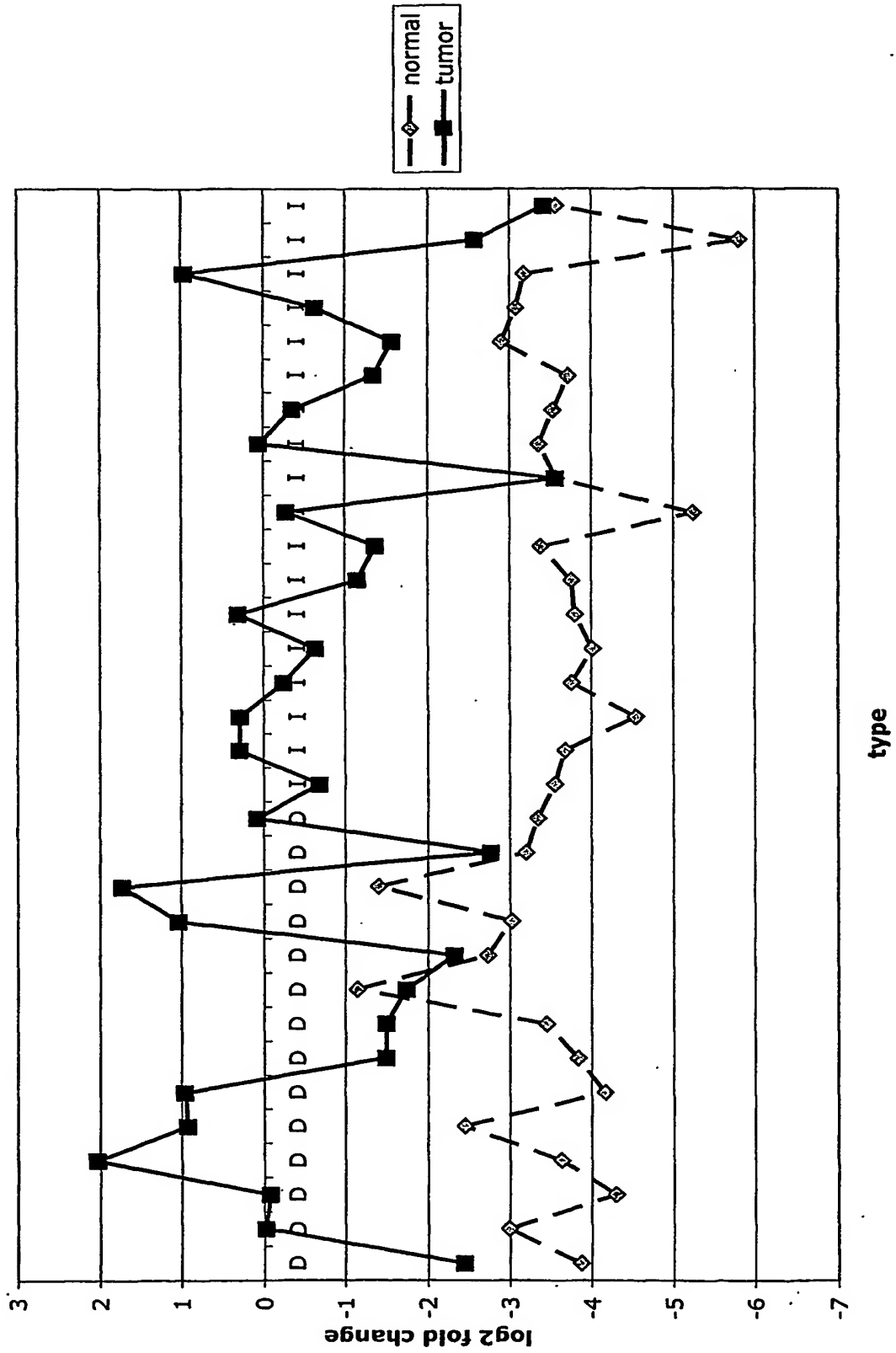


Fig. 11y SERPINH1



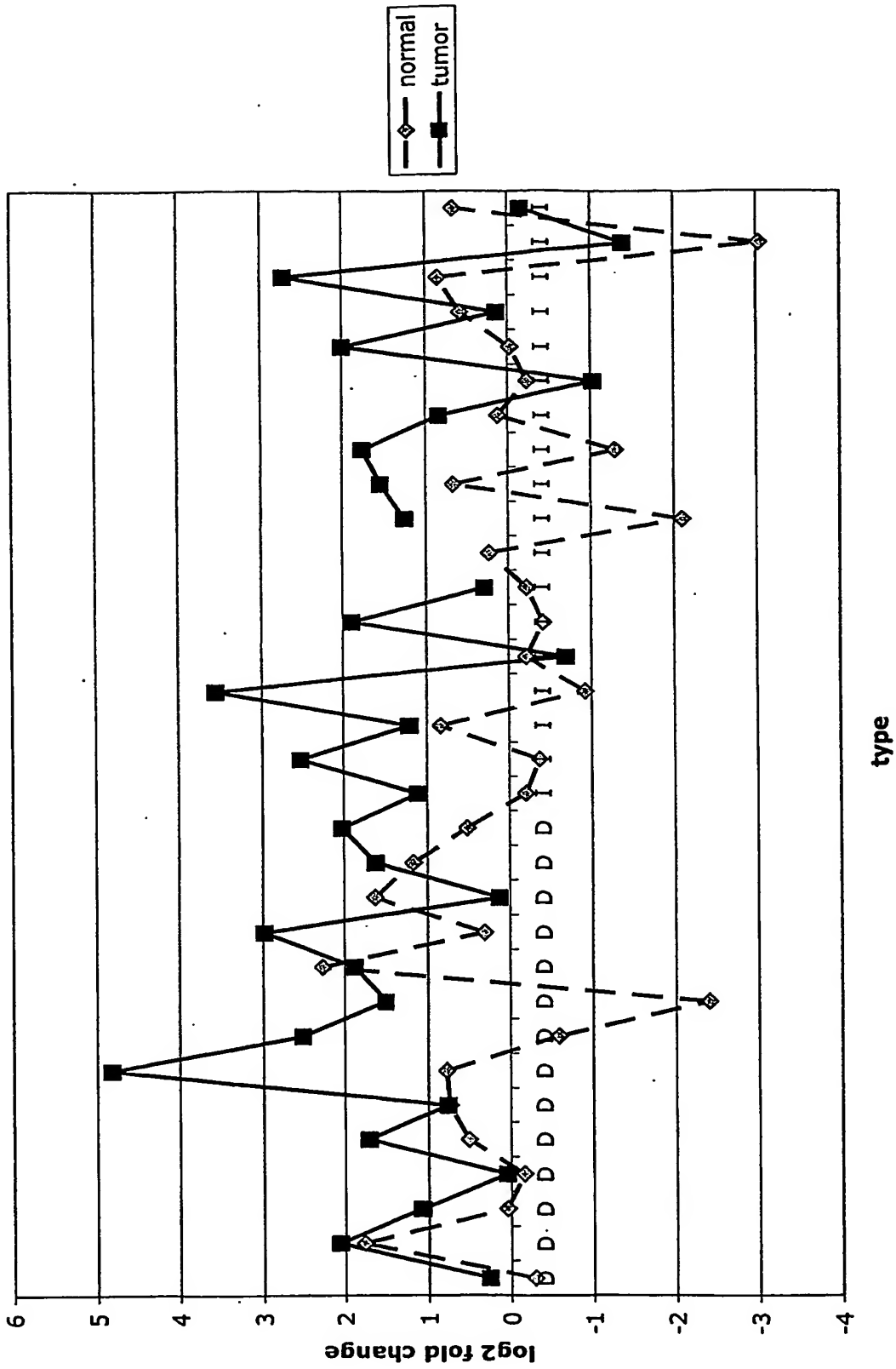


Fig. 11z MMP2

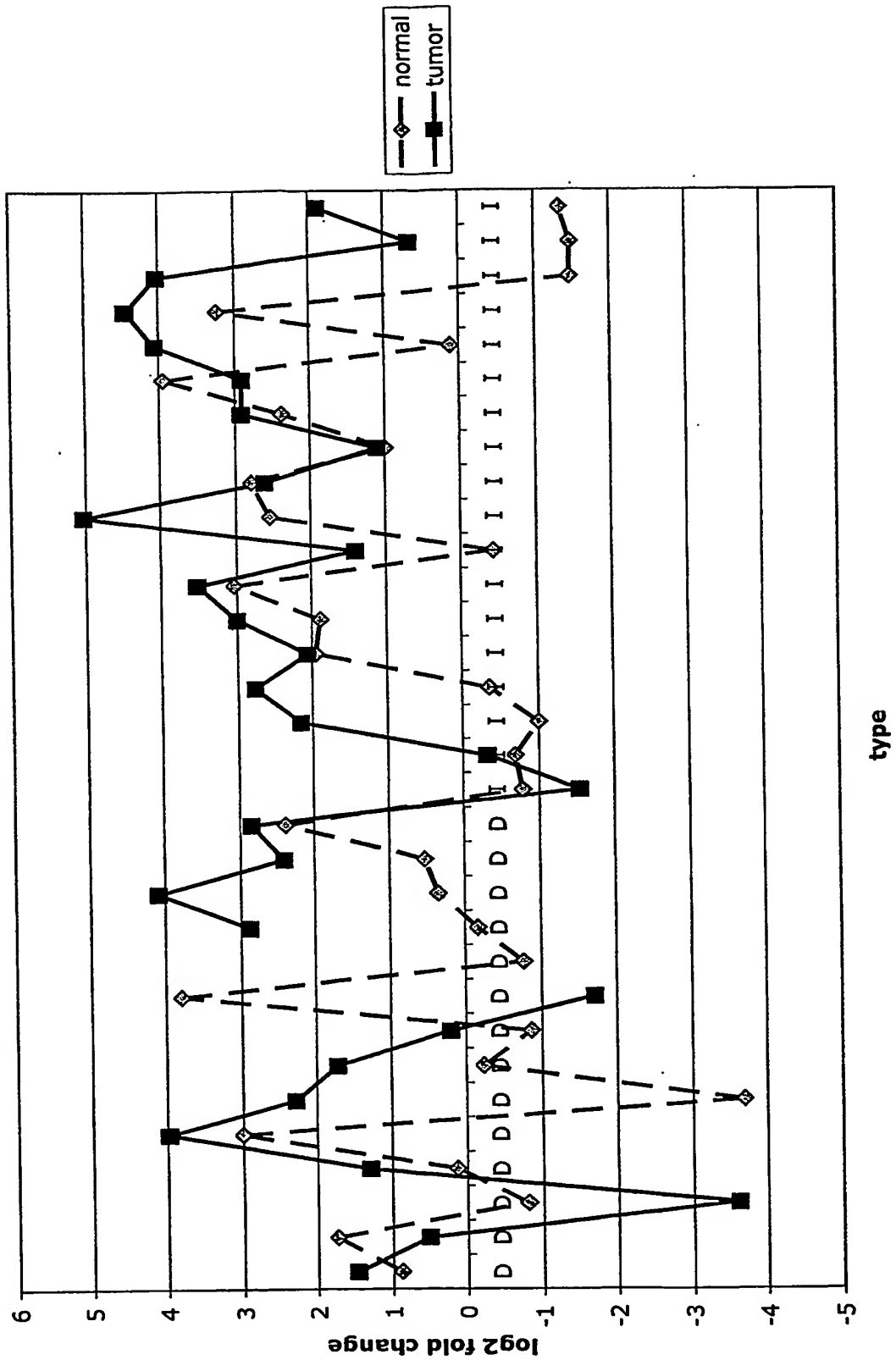
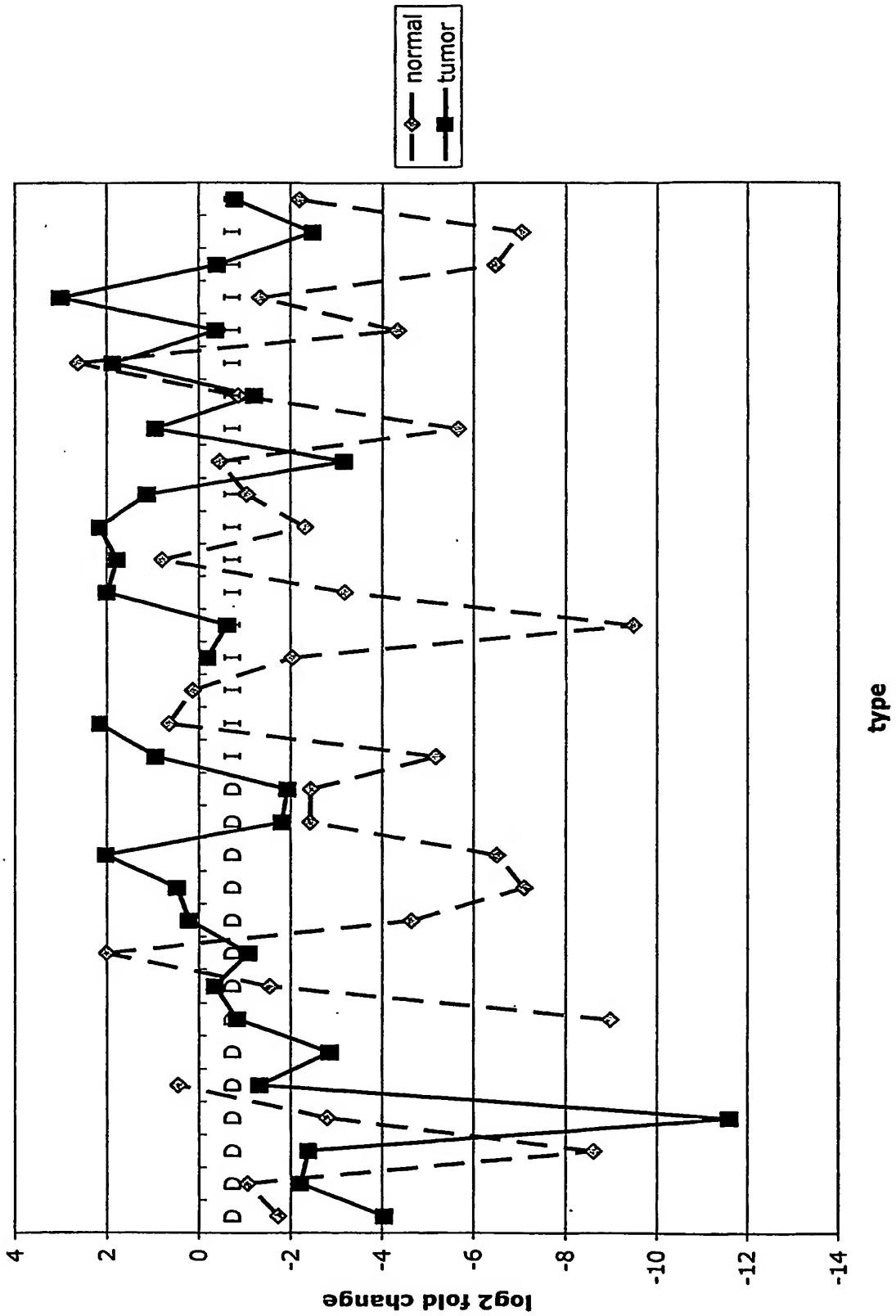


Fig. 11aa PCSK5

Fig. 11ab SERPINB5



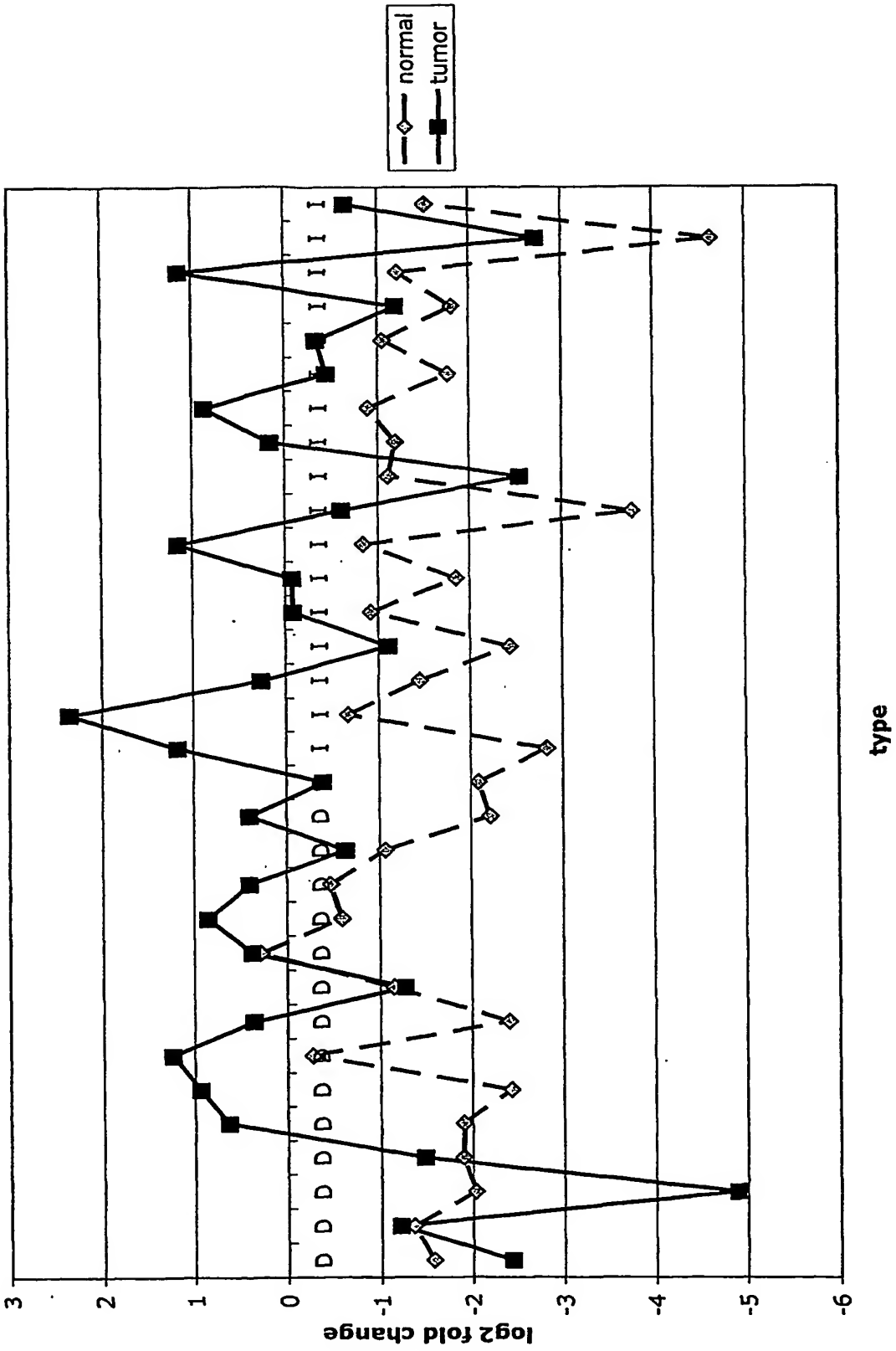
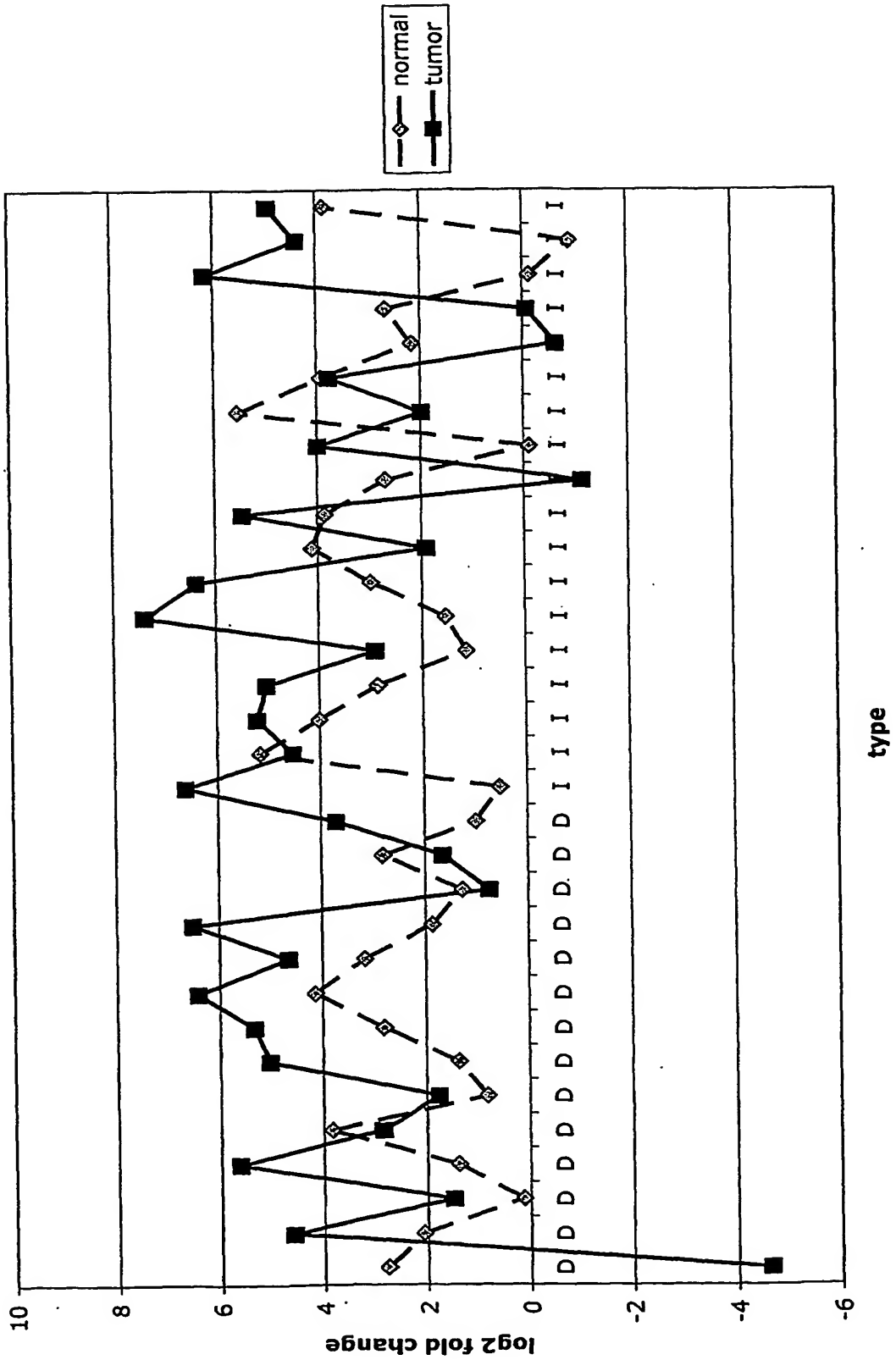


Fig. 11ac TGFB1

Fig. 11ad CEACAM5



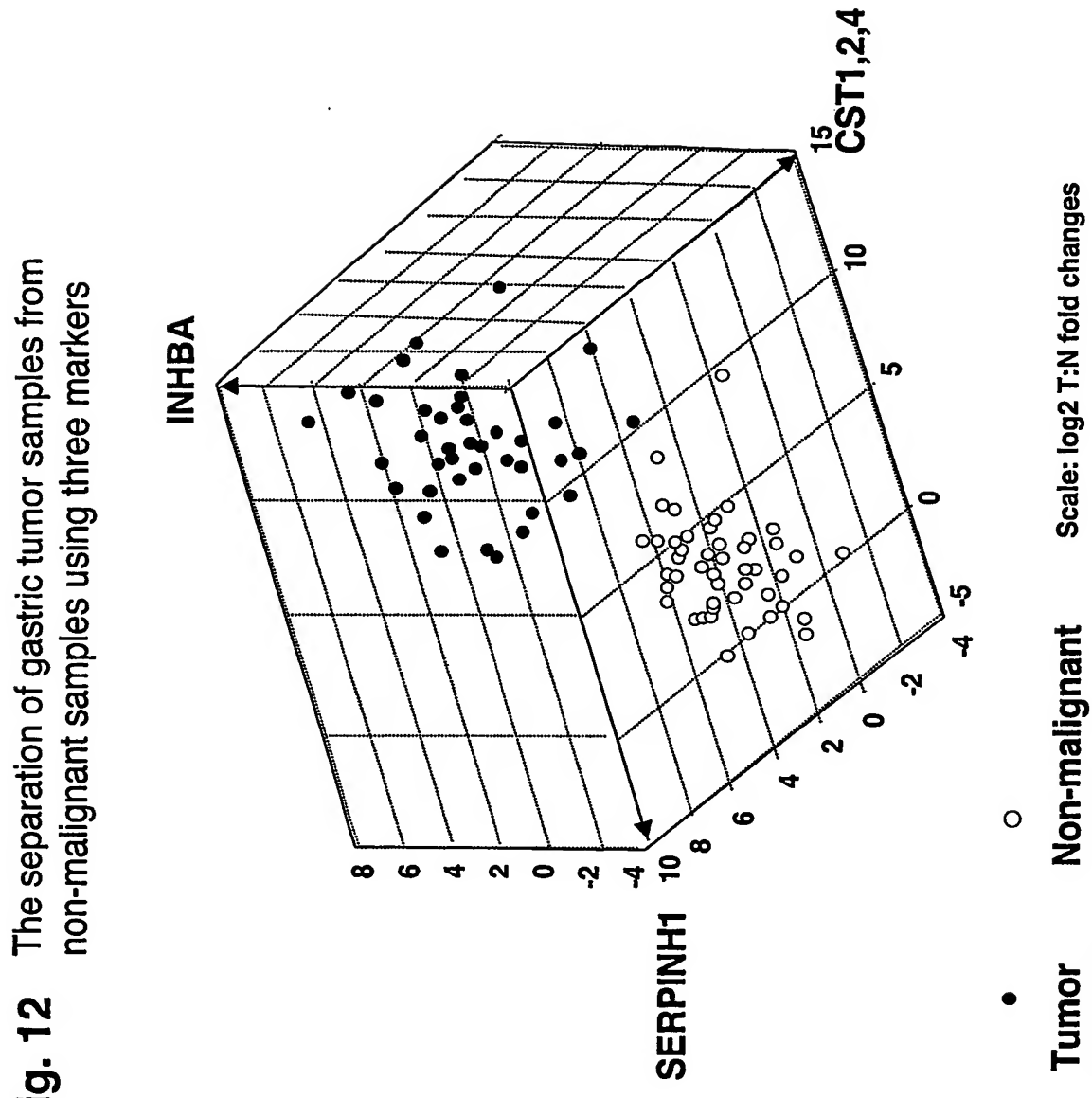


Fig. 12 The separation of gastric tumor samples from non-malignant samples using three markers

Number of markers in test	Total possible tests	Number of tests with sensitivity			Proportion of tests with sensitivity		
		>=90%	>=95%	>=99%	>=90%	>=95%	>=99%
1	29	2	1	0	6.9%	3.4%	0%
2	406	33	27	1	8.1%	6.7%	0.2%
3	3654	796	457	50	21.8%	12.5%	1.4%

Fig. 13. The effect of multiple markers on the ability to accurately discriminate between tumor tissue and non-malignant tissue.

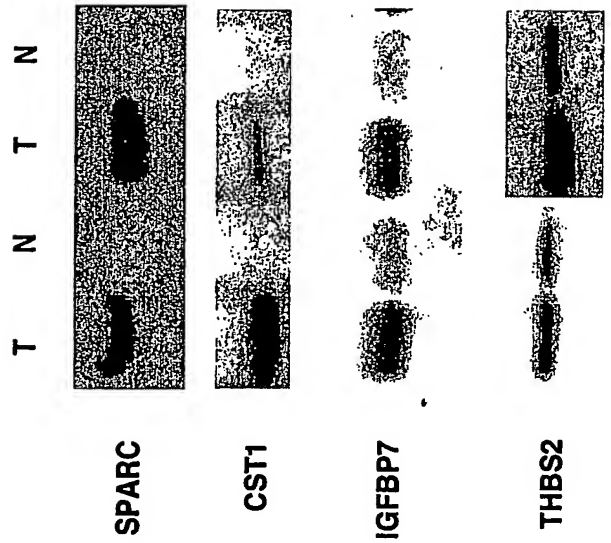


Fig. 14. Western analysis of markers in tumor and non-malignant tissue

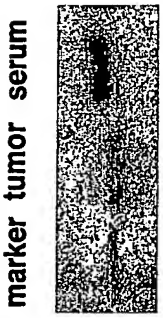


Fig. 15. Western analysis of SPARC in gastric tumor material and serum.

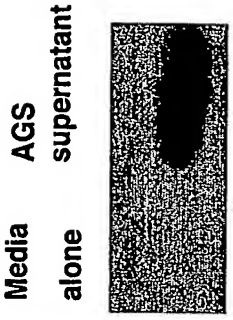


Fig. 16. Immunodetection of cystatin SN in the supernatant of the gastric cancer cell line, AGS.